

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:09:25 ; Search time 24.8 Seconds  
(without alignments)  
1314.204 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292

Sequence: 1 MVEPGPTANSTPMGAGPP.....FNIDPAPELRLPHLGIPFN 440

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A\_Geneseq\_1101.\*

1: /SID8/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /SID8/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
4: /SID8/gcgdata/geneseq/geneseqp/AA1983.DAT.\*  
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6: /SID8/gcgdata/geneseq/geneseqp/AA1985.DAT.\*  
7: /SID8/gcgdata/geneseq/geneseqp/AA1986.DAT.\*  
8: /SID8/gcgdata/geneseq/geneseqp/AA1987.DAT.\*  
9: /SID8/gcgdata/geneseq/geneseqp/AA1988.DAT.\*  
10: /SID8/gcgdata/geneseq/geneseqp/AA1989.DAT.\*  
11: /SID8/gcgdata/geneseq/geneseqp/AA1990.DAT.\*  
12: /SID8/gcgdata/geneseq/geneseqp/AA1991.DAT.\*  
13: /SID8/gcgdata/geneseq/geneseqp/AA1992.DAT.\*  
14: /SID8/gcgdata/geneseq/geneseqp/AA1993.DAT.\*  
15: /SID8/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
16: /SID8/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /SID8/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /SID8/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /SID8/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1893.5	82.6	437	14	AA19801
2	561	24.5	477	22	AA19765
3	558.5	24.4	405	19	AA19333
4	557.5	24.3	400	14	AA19501
5	557.5	24.3	466	13	AA19505
6	554	24.2	405	15	AA19515
7	553.5	24.1	365	20	AA19737
8	552.5	24.1	400	10	AA19592
9	552.5	24.1	446	12	AA19498
10	552.5	24.1	446	14	AA19364
11	546	23.8	388	13	AA19598

12	533.5	23.3	487	18	AA19795	DI dopamine recept
13	531.5	23.2	446	12	AA19549	Rat dopamine DI re
14	531	23.2	402	11	AA196495	Beta 3 adrenergic
15	531	23.2	407	19	AA195847	Human adrenergic b
16	527.5	23.0	408	15	AA195991	Human beta-3 adre
17	527.5	23.0	487	12	AA19596	DI dopamine recept
18	508	22.2	379	18	AA193185	Corn barnacle G-pr
19	507.5	22.1	560	22	AA195666	Rat alpha-1a adren
20	503.5	22.0	565	22	AA195409	Human adrenocept
21	503	21.9	572	12	AA195071	Human alpha-1a adr
22	503	21.9	572	16	AA190039	Human alpha-1a adr
23	503	21.9	572	17	AA195945	Human alpha-1a adr
24	503	21.9	572	17	AA195945	Human alpha-1a adr
25	503	21.9	572	12	AA195662	Human alpha-1a adr
26	500	21.8	572	22	AA195681	Human alpha-1a adr
27	499.5	21.8	501	15	AA197096	Human alpha-1a adr
28	499.5	21.8	501	21	AA195168	Sequence of human
29	494.5	21.6	478	20	AA192853	Active form of hum
30	494.5	21.6	478	22	AA1945805	Human serotonin re
31	493	21.5	515	22	AA195668	Hemster alpha-1b a
32	491.5	21.4	477	13	AA1921082	Dopamine DI recept
33	491.5	21.4	501	16	AA190040	Human alpha-1a adr
34	489.5	21.4	572	15	AA1952830	Sequence of human
35	488	21.3	477	16	AA19381	Dopamine receptor
36	488	21.3	477	18	AA1940802	Human D5 dopamine
37	488	21.3	515	15	AA190995	Human/rat hybrid a
38	488	21.3	515	16	AA190041	Human/rat hybrid a
39	487.5	21.3	475	14	AA1931046	Rat D1B dopamine r
40	486	21.2	515	21	AA1967236	Mouse alpha-1b adr
41	485.5	21.2	501	22	AA195665	Human alpha-1a adr
42	485.5	21.2	515	22	AA1905408	Human adrenocept
43	484	21.1	515	22	AA195667	Rat alpha-1b adren
44	481.5	21.0	377	15	AA194693	G-protein coupled
45	481.5	21.0	377	17	AA1902665	G-protein coupled

#### ALIGNMENTS

RESULT 1	
AA1936801	
ID	AA1936801 standard; Protein: 437 AA.
XX	
AC	AA1936801;
XX	
25-AUG-1993	(first entry)
XX	
DE	Rat serotonin St-B17 receptor.
XX	
KW	Polymerase chain reaction; primer: PCR; amplify: rat; serotonin;
KW	G-protein; receptor: catecholamine; St-B172; St-B17; drug: CNS;
KW	Intron; splice: clone: transmembrane; 5-HT; family: hydrophobic;
KW	5-HT2; 5-HT1D; 5-HT1C; 5-HT1B; 5-HT1A; 5-HT1E.
XX	
OS	Synthetic.
XX	
PN	US7970338-A.
XX	
PD	01-APR-1993.
XX	
PF	26-OCT-1992; 92US-0970338.
XX	
PR	26-OCT-1992; 92US-0970338.
XX	
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX	
PI	Monsma FJ, Sibley DR;
XX	
DR	WPI: 1993-159491/19.
XX	
DR	N-PSDB; AA041701-2.
XX	
PT	Cloned gene encoding serotonin St-B17 receptor gene - used to
PT	test drugs for CNS activity

XX Disclosure; Page 31-33; 51pp; English.  
 CC This sequence encodes the rat serotonin St-B173 receptor and was  
 CC encoded by the clone St-B173. The putative intron, found in clone  
 CC St-B172, was absent from this clone with the flanking exons being  
 CC spliced together at nucleotide 873. Splicing at this position results  
 CC in a 1311 bp open reading frame encoding a protein of 437 amino acids  
 CC with a molecular weight of 46.8 kD. Hydrophobic analysis of this amino  
 CC acid sequence indicated several hydrophobic regions predicted to  
 CC represent putative putative transmembrane spanning domains. When  
 CC compared to previously cloned G-protein coupled receptors, the  
 CC transmembrane regions of St-B17 exhibited high homology to various  
 CC serotonin (5-HT) receptors suggesting that it may be a member of this  
 CC receptor family. Within the transmembrane regions, St-B173, exhibits  
 CC homology of 41%, 39%, 38%, 37% and 36% with 5-HT2, 5-HT1D, 5-HT1C,  
 CC 5-HT1B, 5-HT1A and 5-HT1E receptors respectively. The isolated gene,  
 CC St-B17, encodes a protein which may be used to test CNS activity of  
 CC drug candidates.

Sequence 437 AA;

Query Match 82.6%; Score 1893.5; DB 14; Length 437;  
 Best Local Similarity 84.3%; Pred. No. 8.2e-176;  
 Matches 375; Conservative 11; Mismatches 46; Indels 13; Gaps 4;

1 MYPPGPANTSTPAMGAGPSAPGSGVMAALCVIALTAANSILIALICTOPALRNT 60  
 1 mvppepynsttpawgppppgpggsvaaalcavivltaanaillivllctgpavnt 60  
 61 SNFFLVSLFTSDLVWGLVMPAMLNALYGRWVLARGLCLMTAFDVMCCASILNLCI 120  
 61 snffvlslftsdlvwglvmpamlnalylgrwvlarglclmtafdvccsaslnlcll 120  
 121 SLDRYLLILSLRYKLRMTPLRALALVLAWSLAALSFLLGLGWHRLGHAAPPVGC 180  
 121 sldryllilslryklrmtplralalvlgawslaalsfllglgwhrlghaappvgc 180  
 121 sldryllilslryklrmtplralalvlgawslaalsfllglgwhrlghaappvgc 180  
 181 RLALSLPFLVLAASGLTFELPSGALCFYCRILLAARKOAVASLTGMAASQASETLQVP 240  
 181 rllslpflvlasgltfelpsgalcftycrilllaarkavastltgtaqaletlqvp 240  
 181 rllslpflvlasgltfelpsgalcftycrilllaarkavastltgtaqaletlqvp 240  
 241 RTPPGVESADSRRLAKHRSKALKAKITLGLGMFFVTLPPFVANIVAOVDCDSIPG 300  
 241 rtppgvessadrrlakhrrskalkakitlglgmffvtlppfvanivaovcddcspg 300  
 241 rtppgvessadrrlakhrrskalkakitlglgmffvtlppfvanivaovcddcspg 300  
 301 LFDVLTWIGYNSMTPIYPLFMRDFKRALGRFLPCRCRERQASLASPSL-----RT 355  
 301 lfdvltwlgynsmtpiylplfmrdfkralgrflpcrcrerqaslaspsl-----rt 355  
 301 lfdvltwlgynsmtpiylplfmrdfkralgrflpcrcrerqaslaspsl-----rt 355  
 356 SHSGPRPGLSLQOVLPPLPDSDSAGSGSSGLRLTAQLLPGFATDPPPLPTRA 415  
 356 shsgprpqlslqovlpplpdsdsagsgssglrltaqlllpgfatdppplptraa 415  
 357 qrcqlrp-qgqylalplpnsads--aasgysglqltaqllllpgaatrdppptcat 412  
 416 AAVNFENIDPAEPRLRHPDGIPTN 440  
 416 aavnfenidpaeprlrhpdgipn 440  
 413 tvnfvfivdsvepeirpplsspv 437  
 413 tvnfvfivdsvepeirpplsspv 437

RESULT 2

AAB70765 standard; Protein; 477 AA.

AC AAB70765;

DT 18-MAY-2001 (first entry)

DE Human beta1-adrenoreceptor protein.

KM Beta1-adrenoreceptor; human; mutation; disease predisposition;

KM cardiomyopathy; dilative.

OS Homo sapiens.  
 XX  
 PN W020011039-A2.  
 XX  
 PD 15-FEB-2001.  
 XX  
 PF 04-AUG-2000; 2000WO-DE02648.  
 XX  
 PR 05-AUG-1999; 99DE-1038390.  
 XX  
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
 PI Wallukat G, Podlowski S, Wenzel K, Mueller J;  
 XX  
 DR WPI; 2001-202770/20.  
 XX  
 PT New mutated gene for human beta1-adrenoreceptor, useful for drug  
 PT development and in genotyping for predisposition to cardiomyopathy -  
 XX  
 PS Claim 4; Page 22-23; 23pp; German.

This invention describes a novel human beta1-adrenoreceptor gene (I) that comprises 1-7 or more mutations, excluding the sequence with the mutations Ala145Gly or Gly1165Cys. The invention also describes (1) a method for determining predisposition to disease by genotyping DNA of (1) at one or more exchanged position and comparison with a reference sequence; and (2) a new variant of the beta1-adrenoreceptor (II) which include at least one of the amino acid changes Ser49Gly, Ala55Ser, Gly389Arg, Arg399Cys, His402Arg, Thr404Ala and/or Pro418Ala, but excluding the sequence with a single amino acid exchange at positions 49 or 389. Genotyping of (I) is used to determine predisposition to cardiomyopathy, specifically the dilative form, also for prognosis and assessing severity of this condition. Gene (I) can be used for the following: (i) development of therapeutic agents, especially a new class of beta1-adrenoreceptor (antagonists); (ii) construction of genes or vectors, especially for pharmaceutical development; and (iii) develop diagnostic kits, particularly for determining predisposition and individual responses to different beta1-adrenoreceptor (antagonists, including predisposition to develop side effects and habituation.

Sequence 477 AA;

Query Match 24.5%; Score 561; DB 22; Length 477;  
 Best Local Similarity 34.3%; Pred. NO. 4.6e-46;  
 Matches 148; Conservative 66; Mismatches 161; Indels 56; Gaps 14;

1 MYPPGPANTSTPAMGAGPSAPGSGVMAALCVIALTAANSILIALICTOPALRNT 60  
 1 mvppepynsttpawgppppgpggsvaaalcavivltaanaillivllctgpavnt 60  
 33 lvpasppasllppasegpepigsqtsmgllmalivllvagnvlyvalaktprlqtl 92  
 61 SNFFLVSLFTSDLVWGLVMPAMLNALYGRWVLARGLCLMTAFDVMCCASILNLCI 120  
 61 snffvlslftsdlvwglvmpamlnalylgrwvlarglclmtafdvccsaslnlcll 120  
 93 tnlflmsaasdlvmgllvlpfgatlvwgrwgsffcelwtstvdvlcvastletclvl 152  
 121 SLDRYLLILSLRYKLRMTPLRALALVLAWSLAALSFLLGLG--HELGHARPPV-- 176  
 121 sldryllilslryklrmtplralalvlgawslaalsfllglg--helgharppv-- 176  
 153 aldrylaltspfygsltrrararglvtcwaalsalvsflpilmhwaesdearcynd 212  
 177 PGCCRLASLPFLVLAASGLTFELPSGALCFYCRILLAARKOAVASLTGMAASQ 232  
 177 pgccrllaslpflvlasgltfelpsgalcftycrilllaarkoavasl--ltgmasq 232  
 213 pkccdfvunrayaiaassvstfypdclmatytlvfreagqyvkldscerrflfgparr 272  
 233 ASFT-----LQVPRTPGVESADS-----RRLATKHSRKALKARLTGIL 273  
 233 asft-----lqvprtpgvessads-----rrlatkhsrkalkarltgilt 273  
 273 pspspypappppppppaaataatpangragkrtrprlvalreqkalk-----tlgil 329  
 274 LGMFFVTLPPFVANIVAOV--CDCISPGLPDVTWLGVCNSTMNPITY--PLFMRDFKR 329  
 274 lgmffvtlppfvanivao--cdcispglpdvtwlgvcnstmnpity--plfmrdfkr 329  
 330 mgvftlcwlpfflanvkafrrelvdpdlffvfmwllgyanaafnilycrsp---dfirk 385  
 330 mgvftlcwlpfflanvkafrrelvdpdlffvfmwllgyanaafnilycrsp---dfirk 385  
 330 algrflpcpr---cprerqaslaspslrltsrsgprgls--lqovlpplp--pdsdSD 383  
 330 algrflpcpr---cprerqaslaspslrltsrsgprgls--lqovlpplp--pdsdSD 383

DB 386 atgfc1lccarractr-----raah-gdiprasgclaragpppsgaasddddd 433  
 QY 384 AGSGSGSSGLRL 394  
 DB 434 dvvgatcparrl 444

## RESULT 3

AAW44933  
 ID AAW44933 standard; Protein: 405 AA.

AC AAW44933;

DT 14-OCT-1998 (first entry)

DE Canine beta-3 adrenergic receptor.

KW Canine; beta-adrenergic receptor; brown adipose tissue; probe; human;  
 hybridisation; ligand; ss.

XX Canis familiaris.

EH Key Location/Qualifiers

FT Modified-site 8..10

FT /note= "Asn is N-glycosylated"

FT Modified-site 26..28

FT /note= "Asn is N-glycosylated"

FT Domain 38..63

FT /label= transmembrane domain 1

FT Domain 76..99

FT /label= transmembrane domain 2

FT Domain 110..131

FT /label= transmembrane domain 3

FT Domain 156..178

FT /label= transmembrane domain 4

FT Domain 203..226

FT /label= transmembrane domain 5

FT Domain 293..314

FT /label= transmembrane domain 6

FT Domain 322..347

FT /label= transmembrane domain 7

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

CC e.g. diabetes. The canine version of RA-Ca-b3 can be used to develop  
 CC treatments specific for dogs. The sequence can also be used in the beta-2  
 CC differential screening for ligands for RA-Ca-b3 as compared to the beta-2  
 CC adrenergic receptor (AAW44932).  
 XX  
 SQ Sequence 405 AA;

Query Match 24.4%; Score 558.5; DB 19; Length 405;  
 Best Local Similarity 35.6%; Pred. No. 6.5e-46;  
 Matches 148; Conservative 59; Mismatches 154; Indels 55; Gaps 15;

QY 3 PEGPTANSTPAMGAGPPSPGSGGWAALCVIALTAANSLIALCTQPALRNTSN 62  
 DB 18 PGPpdaant-----s9lpapawavalagallalevalatvgnllyvalartprlqumcn 73  
 QY 63 PFLVSLFTSDLVWGLVMPVPMALNLYGHWVALRGICLMTAFDWCSSASTLNLCLISL 122  
 DB 74 vftstlatadlvvglllvppgatlatlgtwpgatgcetwsvdvlcvstasietlcalav 133  
 QY 123 DRYLLILSPLRKRLRMTPLRALALVGAWSLAALASFLPLLGMELG-----HARP 174  
 DB 134 drylavtnplrygalvltkraraavvlwvsaavsfapimskwrvygaadaeqchsnp 193  
 QY 175 PVPGCCRLASLPVLVAGSLPFLPSGALCFTYCHILAAKQAOVQVASTLTGMASQAS 234  
 DB 194 hc-----cafasnlpayallssvsfypdllymlyvatvrlvatcrg-rlrlrlrelgrfppe 249  
 QY 235 ETLQVPRPRPG-----VESADSR--RLATKHSRKALAKLTLGLGMFEVWL 282  
 DB 250 sppaasrtrspgparrrcaapaavpdrllrparllprehralr---lglvgftlcwl 306  
 QY 283 PRFVANIVQAVCD---CISPGLEFVLTWLGYNSTMNPIIY---PLFMRDKRALGRFP 336  
 DB 307 pftvanvmtalgpslvpsall-almwlgynasfnpllycrsp---dftsatfrll- 360  
 QY 337 CPRCPREQASLASPSLRTSHSGPRGLSLQOVLPLPLPPDSUSDSDAGSGSSGL 392  
 DB 361 c-rrtreehraaasp-----p9dpsaapaaltspaes-srocaidgaswyl 404

## RESULT 4

AAAR32501  
 ID AAR32501 standard; Protein: 400 AA.

AC AAR32501;

DT 09-JUN-1993 (first entry)

DE Beta-adrenergic receptor.

KW Fat cell specific; BAR; lipolysis; obesity; diagnosis;

KW thermogenesis; metabolism.

OS Rattus rattus.

PN US7783602-A.

PD 15-DEC-1992.

PF 11-NOV-1991; 91US-0783602.

PR 01-NOV-1991; 91US-0783602.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.

PI Venter CJ;

DR WPI; 1993-067426/08.

XX Fat cell specific beta- adrenergic receptor polypeptide - used  
 PT for diagnosis of obesity due to inactive lipolysis  
 XX

Disclosure; Page 16; 20pp; English.

A rat intraparticular brown adipose tissue cDNA library was cloned and probed with DNA probes encoding human beta-1 and rat beta-2 adrenergic receptors under low stringency conditions. Positive clones were found to be different from the rat and human sequences and contained a single open reading frame of 1200 bp encoding the protein shown, of 400 amino acids and mol. wt. 43 kD. The protein is the fat specific beta-adrenergic receptor and may be used in work on the thermogenesis process. Isolation of the gene for RAR allows the diagnosis and treatment of obesity and the testing of medications for their effectiveness in stimulating the thermogenesis metabolic response in obesity patients.

Sequence 400 AA;

Query Match	24.38; Score 557.5; DB 14; Length 400;
-------------	--

Best Local Similarity 36.0%; Pred. NO. 8e-46;  
Matches 145; Conservative 61; Mismatches 144; Indels 53; Gaps 16;

QY 5 PGPRANSTPA-WGAGP---PSAPGSGS-----WVAALCVIAL--TAAANSLTALICTQ 54  
3 pwpkngslatwsaprltldpsaantstslgpywaeaalagallatlatvngnllvltatart 62  
Db 3  
QY 55 PALNTSNFELVLSFTSDLMVGLVMPMPAMINALYGRKVTARGLCLLTMTAFDWCCSAST 114  
63 prlqtlnvftstlatadlvglilvmpgpatlatlmpglatgcetlwtstadvclvcasti 122  
Db 63  
QY 115 LNLCLLSIDRYLLLSPLRYKTLKNTPTLRALALVGAANSMAALSFTLLDGLGHELG---- 170  
123 elticalvdrylatnptlryglctlckrtaraavllvaivstsvsfapimqmwvvgadae 182  
Db 123  
QY 171 ----HARPVGQCRLLAS-LPEFLVASGLTFEPPSACICTYCRILLAAKQAVQVASTL 225  
183 aqechsnp-----rcksfasmypyalissvstfyrlpmlvfygarrvtvaktrqr-ftvrr 237  
Db 183  
QY 226 TTGNASQASFTLQVPRTPRP-----GVESADSR--RLATKSRKALKAKTLTGIL 273  
238 elgpatveepsrpsrpsptatvgtfpcasdgpcgrtparrllpighralt--tlgll 294  
Db 238  
QY 274 LGMFFVWMLPRFVANIVQAVC--DCISBGLFDVLTWLGCGKSTNNPLITY---PLFMDFK 322  
295 mglstlcwlpflfanvralvaypsvlvpsgvfiawlnvlgaynsafnpllylcrspdfdrar 354  
Db 295  
QY 329 RAL-----GRFLPCRC---PRERASLASPSLR--TSHSGRP 362  
355 rllcsyggrrgpeeprrvltfsspsvassqnsplnrfdgdyegerr 397

RESULT	5
AAR26505	
ID	AAR26505 standard; Protein; 466 AA

AC AAR26505;

DT 12-FEB-1993 (first entry)

DE Adrenalin receptor subtype beta-1.

KM Drugs; dabutamine; prenalterol; acebutolol; metoprolol; atenolol, KM practolol.

05 Rattus rattus.

PN JP04211374-A.

PD 03-AUG-1992.

PF 15-FEB-1991; 91JP-0044479

PR 27-FEB-1990; 90JP-0048794

PA (SUMU ) SUMITOMO SEIYAKU KK.

DR WPI; 1992-304939/37.  
DR N-PSDB; AAQ27816.

PT DNA encoding adre

PT derived from human adrenalin

PS Disclosure; page 5; 8pp; Japanese.

CC The sequence is useful in studies

cc blocking the receptor, e.g. acebutolol, metoprolol, atenolol or  
cc practolol.

SQ Sequence 466 AA;

Query Match	Score	DB 13	Length
24.3%	557.5	13	166

Best Local Similarity -34.28; Pred. NO. 9.7e-46; ,  
Matches 150; Conservative 63; Mismatches 163; Indels 63; Gaps 15

```

QY 7 PTANSTAWMGPPSSAAGGSSWAA---ALCVIALTAANAISLLIALICTQPAIRRTSNF 63
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 38 ppaalipaseq--sapisqwtetgmgliallivilivgnvivaiaaktprlqtl 95
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 64 FLVALFESDLMWGLVWMPPALNALYGRWVLAROLCLLMAFDWCCSASILINCLISLD 123
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 96 flmslaaadlvmglilvvpfgatlvwrgtweygfscelwtswdvclvdstetclvald,155
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 124 RYLLILSPKRRKRLMTPLRALVALYGMASLAALASFPLLLIGW--HELGHARPPV--PGQ 179
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 156 rlylrsptfrygslllraaraiaivcvaalsavsfllpilmhwraesdearctyodpkc 215
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 180 CRLIASLPEVLVASGLTFPELPGSACIFCYCRILLAAKRAQOVAASLTWGMAS-----QAS 234
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 216 cdfntnetaiaassvsvfypclcmatvylrvfreagkqykklidscerflfsgpprrppsp 275
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 235 ETLOVPRTPRGVSADSR-----RLATKHSKALKAKULTICILIGMFPVWLPFEVA 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 276 apsdpspprpadslangiresaktrpsrlvalreqkalk---tligilngvftlcwfpiflg 332
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 288 NIVQAV--CDICSPGLFVULVGLYGCNSMMPDIY---PLFMRPDRKRLCFGLPCPP--C 340
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 333 nvvaafmndlypdtllyfvmlygransafmilycrsp-----dlrckfqlilccarraac 368
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 341 PREROASLASFLRTSHSG--PRPGLSLQOVLPLPLP--PDSDSDSAG----- 385
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 389 rr-----f-raangdrprasaclaraqppspapsdsdaddadagatpparlllepwa 437
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 386 --SGGSSGLRITAOALLPG 402
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 438 gcngylltvdssdiidp 456
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT	6
AAR62515	
ID	AAR62515 standard; Protein; 405 AA

AC AAR62515;

DT 06-JUL-1995 (first entry)

DE Bovine beta3 adrenergic receptor.

KW bovine; beta3 adrenergic receptor; identification; agonist;  
KW antagonist; regulate fat level; improve meat quality.

OS      Bos taurus

FH	Key	Location/Qualifiers
FT	Region	38..63

```

FT      Region 1 (TM1); see AAR70668"
FT      /note="transmembrane region 1 (TM1); see AAR70668"
FT      76..99
FT      /note="transmembrane region 2 (TM2); see AAR70669"
FT      110..131
FT      Region 3 (TM3); see AAR70670"
FT      /note="transmembrane region 3 (TM3); see AAR70670"
FT      156..178
FT      Region 4 (TM4); see AAR70671"
FT      /note="transmembrane region 4 (TM4); see AAR70671"
FT      203..226
FT      Region 5 (TM5); see AAR70672"
FT      /note="transmembrane region 5 (TM5); see AAR70672"
FT      293..314
FT      Region 6 (TM6); see AAR70673"
FT      /note="transmembrane region 6 (TM6); see AAR70673"
FT      322..347
FT      Region 7 (TM7); see AAR70674"
FT      /note="transmembrane region 7 (TM7); see AAR70674"
XX      MO9424162.A.
XX      27-OCT-1994.
XX      21-APR-1994; 94MO-FR00447.
XX      21-APR-1993; 93FR-0004670.
XX      PA      (VETI-) VETIGEN.
XX      PA      (VETI-) VETIGEN.
XX      P1      Kapoor A, Lenzen G;
XX      DR      WPI: 1994-341770/42.
XX      DR      N-PSDB: AAO74367.
XX      PT      New nucleic acid encoding the bovine beta2 adrenergic receptor -
XX      PT      are related peptide(s), vectors and transformed cells, useful for
XX      PT      identifying specific agonists and antagonists
XX      PS      Claim 16; page 3-5; 52pp; French.
XX      AAAR62315 shows the amino acid sequence of the bovine beta2 adrenergic
XX      CC      receptor encoded by AAQ74367. The peptide contains 7 transmembrane
XX      CC      regions, all of which are claimed individually and are useful for the
XX      CC      generation of probes for screening compounds that have
XX      CC      agonist/antagonist activity to the receptor. (See AAR70668-74). These
XX      CC      probes are specific to the beta2 gene and not to beta1 or beta2 genes.
XX      CC      These cpts. could be used to regulate the level of fat in animals,
XX      CC      partic. for improved meat quality.
XX      Sequence 405 AA:
XX
XX      Query Match 24.2%; Score 554; DB 15; Length 405;
XX      Best Local Similarity 33.6%; Pred. No. 1.8e-45;
XX      Matches 143; Conservative 61; Mismatches 156; Indels 66; Gaps 13,

```

Db		304	CWLPFFVNVVVALGGPSLVSGPFLFALNWLGYANSAFPLIYCTSPDLTSAFRLLICRC	363
Oy		335	LE-----CPCRPERRQASLASLPTSTSHSGPRGSLDQVLPLPPDSDDSDACS	386
Db		364	RPEENLAASPRAAPS-----GAPTALSPAGPMQ-----PPEID-----	398
Oy		387	GGSSGL 392	
Db		399	GASCGL 404	
 RESULT 7 AAV13737 ID AAV13737 standard; Protein; 365 AA. XX AC AAV13737; XX DT 13-SEP-1999 (first entry) XX DE Murine beta-1 adreno-receptor. XX KW Murine beta-1 adreno-receptor. XX Human; amine receptor; recombinant; murine; beta-1 adreno-receptor. OS Mus sp. XX PN US928890-A. XX PD 27-JUL-1999. XX PF 06-JUN-1995; 95US-0467559. XX PR 06-JUN-1995; 95US-0467559. PA (HUMA-) HUMAN GENOME SCI INC. PI Li Y; XX DR WPI; 1999-429497/36. XX XX Human amine receptor polynucleotides, vectors and host cells XX XX Disclosure; Fig 2; 22pp; English. XX XX The invention relates to a human amine receptor polypeptide. Host cells CC transformed with a vector comprising the amine receptor coding sequence CC are used for the recombinant production of the polypeptide. The CC polypeptides are useful for treating conditions related to under- CC expression and over-expression of the human amine receptor. The present CC sequence represents a murine beta-1 adreno-receptor. XX SQ Sequence 365 AA.				
 Query Match 24.1%; Score 553.5; DB 20; Length 365; Best Local Similarity 37.8%; Pred. No.1.7e-45; Matches 137; Conservative 56; Mismatches 134; Indels 35; Gaps 12.				
Oy		7	PPLANSTPMAGACPAPSPAGSGGNVA---ALCVYIALTAANSULLALICTGPALRNTSNF	63
Db		9	PPLAISLIPASEG--SAPISQGVLTAGMGLIVALLVILVVGNVLIVAIAKPRJQLTNL	66
Oy		64	PLVSLETSDLNMGIVVMPPAMLNALTYGRMVNLARGICLTMTATPDMGCCASJLNLCLISLD	123
Db		67	LTLMSASAAILNGMLLVVPFGALIVVGRTWEYSFFCELVTCSVDVLCVASIECLCIAIDL	126
Oy		124	RYLLLSPLRLKRMTPURALVLVGAMSIALASFLPDLTGW--HELGHARPV--PGQ	179
Db		127	RYLATSPTIRYGSILTRARARALVCTWAISAISVFPLIMHWZAESDEARRCYNDPKC	186
Oy		180	CELLASLRPVVLVASCITFPFPGCAICTFYTCRIILLARKAOVYAS----LTMGMASQAS-	234
Db		187	cdfvnraayaiassvsvfyvpdicaiafylvlfreaqkvkdidseerflgparppsp	246

```

YY 235 EQLQVPRPRGCVESADSR-----RLATKHSRKALKKLTGLTGLGFEFTWLPPEFVA 287
Db 247 epspspgppripdadsiangrfskrrpsrivalalegalk---tlgltmgvftlcwlpflia 303.
OY 288 NIVQAV-CDCISPGLEFDVLTWLGYNSTWNPITY--PLFMRDPFKALGRFLPCPR--C 340
Db 304 nvvkaefhndlvpdrlfvffwnvlgynasafnpllycrsp----dftrkafrlllccarraac 359
OY 341 PR 342
Db 360 rr 361

RESULT 8
AAR54992
ID AAR54992 standard; Protein; 400 AA.
XX
XX AAR54992;
XX
XX 23-JAN-1995 (first entry)
DE Murine beta-3 adrenergic receptor.
XX
XX Receptor; beta; adrenergic; testing; screening; identification;
KW drugs; adenylate cyclase; hormone; lipase; signal transduction.
XX
XX Mus musculus.
XX
XX EP600136-A.
XX
XX 08-JUN-1994.
XX
XX 01-DEC-1992; 92EP-0403248.
XX
XX PR 01-DEC-1992; 92EP-0403248.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Emorine L, Nahmias-kaminski C, Strosberg AD;
XX
XX WPI: 1994-177542/22.
XX
XX N-PSDB; AA065477.
XX
XX
XX Isolated and purified polypeptides having beta3-adrenergic
XX receptor activity - are used to study the effects of various
XX chemical agents on the beta3-adrenergic receptor
XX
XX Claim 2; Figure 4; 15pp; English.
XX
XX The coding sequence of the beta-three adrenergic receptor can be
XX used in expression vectors which are then used to transform cells.
XX The cells then express the receptor on their surfaces and can be
XX used to study the effects of various chemical agents on the receptor
XX which is coupled to adenylate cyclase and hormone sensitive lipases.
XX
XX
XX Sequence 400 AA;

Query Match 24.1%; Score 552.5; DB 15; Length 400;
Best Local Similarity 35.1%; Pred. No. 2.4e-45;
Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15

OY 5 PGPRTNSRPA-NGACP---PSAPGSGS-----WVAALCQVIAL-TAANSLLIALICQ 54
Db 3 pwpnhngslalsadpdlpsaantsqlypypwaaalagallalaltvgsnllvllaiart 62
OY 55 PALRMTSNFEVLSFTSDLMVGLVYVMPAAMLALYGRWVLARGCLLMTAFDVMCCSASI 114
Db 63 plgltgnifvcslaaadvlgvlvmpgatalcghwplgltgcelsvsgdvltcvtsai 122
OY 115 LNLCLISDRYLLISPLRYKLRMPRLARLALVLCGWSLAFLPLLLGHNHG- 170

```

QY	171	----	HARPVVGQGRCLASLPFVLVAGLTFPLPSGALICTFYCILILAAKQAVQVNSLT	226
Db	123	etlcalavdrylawnlpjryllvtckrrraavlwivsaavsfpapmsqmwrvvgadae	162	
QY	171	---- <th>HARPVVGQGRCLASLPFVLVAGLTFPLPSGALICTFYCILILAAKQAVQVNSLT</th> <th>226</th>	HARPVVGQGRCLASLPFVLVAGLTFPLPSGALICTFYCILILAAKQAVQVNSLT	226
Db	183	aqechsnprc---csfasimpyallsssvstlylpjlmvltyavrvvakrrqr-hllrr	238	
QY	227	TGMASSQASETLQVRETRP-----	GESADSR--PLATKHSRKALKAKLTGLL	274
Db	239	lgrtspespspspspspspspatagtgtpaadpdyppcgrrrrpallplrrhrallr-----tlglim	295	
QY	275	GMEFVTLPLPFVANIVQAVC--DCISGLDEVLTLWLCYSTNMPILY---	PLFMRDFKR	329
Db	296	gfislcwlpffllavitalagpslvpsgvfialnmlyghansafnpvlycrspsdfdafr	355	
QY	330	AL----	GRFLPCPRC---PREQASLASPSLR--TSSGGRP	362
Db	356	llcsygrtgrgeepreavtcfpspsvearspplnrtidyegarp	397	
RESULT	9			1
AA	AA15498			
ID	AA15498	standard; Protein; 446 AA.		
XX	AA15498;			
AC	08-MAR-1992	(first entry)		
DT	Human dopamine D1 receptor.			
DE				
XX	catecholamine; G-protein-coupled receptor; neurotransmitter;			
KW	adenylyl cyclase stimulation.			
XX	Homo sapiens.			
OS				
XX				
XX				
Key	Location/Qualifiers			
FT	Modified-site	5	/label= OTHER	
FT			/note= "N-glycosylation site - putative"	
FT	Modified-site	175	/label= OTHER	
FT			/note= "N-glycosylation site - putative"	
FT	Domain	23..49	/label= transmembrane	
FT			/note= "I"	
FT	Domain	62..87	/label= transmembrane	
FT			/note= "II"	
FT	Domain	94..120	/label= transmembrane	
FT			/note= "III"	
FT	Domain	138..164	/label= transmembrane	
FT			/note= "IV"	
FT	Domain	192..218	/label= transmembrane	
FT			/note= "V"	
FT	Domain	273..299	/label= transmembrane	
FT			/note= "VI"	
FT	Domain	311..337	/label= transmembrane	
FT			/note= "VII"	
FT	Region	265..268	/label= Protein_kinase_A_phosphorylation_site	
FT			/note= "putative"	
FT	Region	338..343	/label= Protein_kinase_A_phosphorylation_site	
FT			/note= "putative"	
XX	WC09118005-A.			
XX	28-NOV-1991.			
XX				



Query Match	23.8%	Score 546	DB 13	Length 388
Db	300	sgetpfcldstntfvtfwfgwanslnpily-afnadfrkafstllgcyrlcpatnna	358	
Qy	347	-----SLASPSLRTHSGRPRELSTIQYVLPPLPPDSOSDAGSGSGRLTAQLLP	401	
Db	359	etvsinnngaaafshbprgsisrscnclvy1lphayssedllkkaaaiarplekisp	418	
Qy	402	GEATQDPLPTRAAAVNFENIDPEKPLRP-----HP	434	
Db	419	-----alsvlldydtctvslekigpiltngqhp	445	
RESULT	11			
ID	AAR25698			
XX	AAR25698 standard; Protein; 388 AA.			
XX	AAR25698;			
XX	20-JAN-1993 (first entry)			
XX	Murine adrenergic beta-3 receptor.			
XX	Mouse; polymerase chain reaction; transmembrane region;			
KW	adrenergic receptor.			
XX	Synthetic.			
OS				
XX	Key	Location/Qualifiers		
XX	Domain	36..60		
XX	Domain	/label= transmembrane		
XX	Domain	70..97		
XX	Domain	/label= transmembrane		
XX	Domain	110..129		
XX	Domain	/label= transmembrane		
XX	Domain	153..175		
XX	Domain	/label= transmembrane		
XX	Domain	201..222		
XX	Domain	/label= transmembrane		
XX	Domain	290..311		
XX	Domain	/label= transmembrane		
XX	Domain	324..344		
XX	Domain	/label= transmembrane		
XX	MO9212246-A.			
XX	23-JUL-1992.			
XX	14-JAN-1992;	92WO-FR00023.		
XX	14-JAN-1991;	91FR-0000320.		
XX	(CNRS ) CNRS CENT NAT RECH SCL.			
XX	Emorine LJ, Nahmias C, Strosberg AD;			
XX	WPI: 1992-268668/32.			
XX	N-PSDB; AAQ26808.			
XX	Murine adrenergic beta-3-receptor and nucleic acid encoding it -			
XX	for treating diabetes, obesity and hyperlipidaemia, and also for			
XX	identifying ligands with beta-3 affinity			
XX	Claim 13; Page 37; 6Lpp: French.			
XX	The murine beta-3 adrenergic receptor gene encodes a polypeptide			
XX	with 82% homology with the human beta-3 adrenergic receptor. The			
XX	CC homology is concentrated in the 7 transmembrane domains.			
XX	See also AAQ26804-7.			
XX	Sequence	388 AA;		

[illegible]

RESULT	12	
AAW09795		
ID	AAW09795	standard; Protein: 487 AA.
XX		
AC	AAW09795;	
XX		
DT	11-JUN-1997	(first entry)
XX		
DE	D1 dopamine receptor.	
XX		
KW	D1 dopamine receptor; activation; adenylyl cyclase activity; coupled;	
KW	guanine nucleotide binding regulatory protein; drug assessment; agonist;	
KW	antagonist; efficacy; affinity.	
XX		
OS	Rattus rattus.	
XX		
Key	Location/Qualifiers	
FF	45	
FT	Modified-site	
FT	/note="N-linked glycosylation site"	
XX		
PN	US5610282-A.	
XX		
PD	11-MAR-1997.	
XX		
PF	06-JUL-1990;	90US-0548714.
XX		
PR	06-JUL-1990;	90US-0548714.
PR	11-MAR-1993;	93US-0029917.
PR	19-MAY-1995;	95US-0444734.
XX		
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	
XX		
PI	Mahan LC, Mcvittie LD, Monsma FJ, Sibley DR;	
XX		
DR	WPI; 1997-178452/16.	
DR	N-PSDB; AAT63657.	
XX		
PT	DNA encoding D1 dopamine receptor protein - for production of	
PT	transformed cells used for drug screening	
XX		
PS	Claim 1; Column 11-16; 24pp; English.	



XX The sequence is the rat D1 dopamine receptor protein which is linked to  
 CC the activation of adenylyl cyclase activity. The receptor also couples  
 CC with guanine nucleotide binding regulatory (G) proteins. By constructing  
 CC cell lines that express the D1 receptor, the affinities and efficacies of  
 CC agonist and antagonist drugs can be assessed.

XX Sequence 487 AA;

Query Match 23.3%; Score 533.5; DB 18; Length 487;  
 Best Local Similarity 33.3%; Pred. No. 2.2e-43;  
 Matches 134; Conservative 72; Mismatches 157; Indels 39; Gaps 12;

OY 30 AALCVIALTRAANSLIALICTOPALRN-TSNFELVSLTSDMLVGLVMPRLNAL 88  
 Db 67 acfslillstlgnltvcaavifrlrskvtnltfvislavsdllyavlympwkavaei 126  
 OY 89 YGRWVLARGLCILMTAPDVMCCSAILNCLISDRYLLISPLRYKLRMTPLRALAVL 148  
 Db 127 agfwpfpg-fpfnlwaifimcstaslnlcvlsvdrwaisspfigyerkmpkaafllis 185  
 OY 149 GAWSLAALASEFLPLLGMHELGHARP--PVPG-----OCRLASLPFVLVASGL 195  
 Db 186 vawtlsvlslfipyqlswkh--aktpwldgntfsltdeddnodttrlsrtyaissai 242  
 OY 196 TEFILPSGALICTYCRILLAARKQAVQASL-TTGASQASSETLQVPRPRGVEASDRR 254  
 Db 243 stfypvalmivtyslrylaqgqirrisaleraavhancqltagngnpvcaqsssfk 302  
 OY 255 LATHSRKALAKLTGILGMEFTWLPFFVANIQAQCD-----CISPGLEFDVLTW 307  
 Db 303 msfkrctkvk---tlavimgvfvcwlpffisncmwpfcgseeqpciclsitdvtw 359  
 OY 308 LGYCNSTWNPITLYPLFMDERKALGRFLPCPR-CPRERQASIASPSLR-----TSHSG 359  
 Db 360 fgwanssimplly-afnadfkafstllgyrlcptlna-letvsinnngavvsshe 417  
 OY 360 PRPGSLDQVLPPLPPSDSDSAGSGGSLRLTAQLLP 401  
 Db 418 prgsiskdcnlvyliphavgsedlkkeeaaglakplekisp 459

# RESULT 13

AAR15499  
 ID AAR15499 standard; Protein; 446 AA.

AC AAR15499;

08-MAR-1992 (first entry)

Rat dopamine D1 receptor.

catecholamine; G-protein-coupled receptor; neurotransmitter;  
 adenylyl cyclase stimulation.

Rattus rattus.

XX Key Location/Qualifiers  
 FH 4 /label= OTHER  
 FT Modified-site /note= "N-glycosylation site - putative"  
 FT 174 /label= OTHER  
 FT Modified-site /note= "N-glycosylation site - putative"  
 FT 135 /label= Protein\_kinase\_A\_phosphorylation\_site  
 FT Modified-site /note= "putative"  
 FT 229 /label= Protein\_kinase\_A\_phosphorylation\_site  
 FT Modified-site /note= "putative"  
 FT 268 /label= Protein\_kinase\_A\_phosphorylation\_site  
 FT Modified-site

FT /note= "putative"

XX M09118005-A.

XX 28-NOV-1991.

XX 13-MAY-1991; 91WO-US03308.

XX 17-SEP-1990; 90US-0583852.

XX 14-MAY-1990; 90US-0523237.

XX (UYDU-) DUKE UNIV.

XX (UYDU-) OREGON HEALTH SCI UNIV.

XX Bunzow JR, Civelli O, Grandy DK, Zhou OY, Caron MG;

XX Dearry A, Falardeau P, Gingrich JA;

XX WPI; 1991-369177/50.

XX N-PSDB; AAQ14955.

XX Example 9; Fig 3A; 52pp; English.

CC The D1 dopamine receptor sequence was obtained from two overlapping  
 CC clones, one genomic and the other from a rat striatum cDNA  
 CC library. The amino acid sequence was deduced from the  
 CC nucleotide coding sequence. The receptor is similar to the human D1  
 CC dopamine receptor (see AAR15498) and known G-protein coupled proteins,  
 CC e.g. Cys(351) in the carboxyl terminus is conserved in most G-protein  
 CC coupled receptors; it may be palmitoylated. The carboxyl tail also  
 CC contains several putative sites for phosphorylation by an agonist-  
 CC dependent receptor kinase.

XX Sequence 446 AA;

Query Match 23.2%; Score 531.5; DB 12; Length 446;  
 Best Local Similarity 33.1%; Pred. No. 3.1e-43;  
 Matches 133; Conservative 72; Mismatches 158; Indels 39; Gaps 12;

OY 30 AALCVIALTRAANSLIALICTOPALRN-TSNFELVSLTSDMLVGLVMPRLNAL 88  
 Db 26 acfslillstlgnltvcaavifrlrskvtnltfvislavsdllyavlympwkavaei 85  
 OY 89 YGRWVLARGLCILMTAPDVMCCSAILNCLISDRYLLISPLRYKLRMTPLRALAVL 148  
 Db 86 agfwpfpg-fpfnlwaifimcstaslnlcvlsvdrwaisspfigyerkmpkaafllis 144  
 OY 149 GAWSLAALASEFLPLLGMHELGHARP--PVPG-----OCRLASLPFVLVASGL 195  
 Db 145 vawtlsvlslfipyqlswkh--aktpwldgntfsltdeddnodttrlsrtyaissai 201  
 OY 196 TEFILPSGALICTYCRILLAARKQAVQASL-TTGASQASSETLQVPRPRGVEASDRR 254  
 Db 202 stfypvalmivtyslrylaqgqirrisaleraavhancqltagngnpvcaqsssfk 261  
 OY 255 LATHSRKALAKLTGILGMEFTWLPFFVANIQAQCD-----CISPGLEFDVLTW 307  
 Db 262 msfkrctkvk---tlavimgvfvcwlpffisncmwpfcgseeqpciclsitdvtw 318  
 OY 308 LGYCNSTWNPITLYPLFMDERKALGRFLPCPR-CPRERQASIASPSLR-----TSHSG 359  
 Db 319 fgwanssimplly-afnadfkafstllgyrlcptlna-letvsinnngavvsshe 376  
 OY 360 PRPGSLDQVLPPLPPSDSDSAGSGGSLRLTAQLLP 401  
 Db 377 prgsiskdcnlvyliphavgsedlkkeeaaglakplekisp 418

# RESULT 14



```
Db 70 mhnvfvtslaaadtvmgllvypaactlaltghmpigatgcclwtsvdvlcvrasietlca 129
OY 120 ISLDRIYLLISPLRYKLNMTPLRLALALVIGANSLAALASFPLLLGWHELG-----H 171
Db 130 lavdiylavtnplrygalvtkrcartavvlwvvsaaavsfapimsqwtvrgadaeaqrch 189
OY 172 ARPPVGGCRLIASLPFVLVVASGLTFEPLPSGACICTYCRILLAAARKQAVQVASTLTGMAS 231
Db 190 snprc---cafasmpryvlsssvsfylpdlvmlfyarvfvatrq---lrlrgelg 242
OY 232 Q--ASETLOVPR-----TPRPGVESADSR--RLATKHSRKALKAKLTGLGILGM 276
Db 243 rfppeesppaprsiapapvytcappegypacgrrparllplrehral---ctlgimgt 299
OY 277 FFVWMLPFFVANIVQAV-CDCTSPG-LFDVLTWLGVCNSTMNPITY---PLFMRDFKRAL 331
Db 300 flcwlplfflanvtralggpslvpgpatfialnwlgyansafnpllycrspdfirsaftrll 359
OY 332 ---GRFLPCPRCPREROASLAS--PSLRTSHSGPR 361
Db 360 crcgrrlppepcaarpalfpsgyparsspaqr 394
```

Search completed: March 15, 2002, 14:11:21  
Job time: 116 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:10:55 ; Search time 13.3 Seconds  
(without alignments)  
1212.972 Million cell updates/sec

Title: US-09-826-509-449  
Perfect score: 2292  
Sequence: 1 MVPEPGPTANSTPMAGAP.....FNIDPAPELPHPLGIPTN 440

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	2287	99.8	440	5H6_HUMAN	P50406 homo sapien
2	1989	86.8	440	5H6_MOUSE	Q91C88 mus musculu
3	1678	73.2	436	5H6_RAT	P31388 rattus norv
4	591.5	25.8	466	BIAR_MOUSE	P34971 mus musculu
5	587.5	25.6	473	BIAR_CANFA	P79148 canis fami
6	586.5	25.6	466	BIAR_RAT	P18090 rattus norv
7	571	24.9	474	BIAR_FELCA	Q91C66 felis silve
8	563.5	24.6	480	BIAR_MACMU	P47899 macaca mula
9	559	24.4	468	BIAR_PIG	Q28998 sus scrofa
10	558.5	24.4	405	BIAR_CANFA	Q02662 canis fami
11	557.5	24.3	467	BIAR_BOVIN	Q91E96 bos taurus
12	557	24.3	477	BIAR_HUMAN	P08588 homo sapien
13	554	24.2	405	BIAR_BOVIN	P46526 bos taurus
14	553.5	24.1	400	BIAR_SHEEP	Q9X158 ovis aries
15	552.5	24.1	400	BIAR_MOUSE	P25962 mus musculu
16	552.5	24.1	446	DADR_HUMAN	P21728 homo sapien
17	552.5	24.1	467	BIAR_SHEEP	Q28927 ovis aries
18	551.5	24.1	400	BIAR_RAT	P26355 rattus norv
19	550.5	24.0	405	BIAR_CAPHI	Q9X157 capra hircu
20	548.5	23.9	466	DADR_MACMU	Q77680 macaca mula
21	547.5	23.9	363	DADR_CARAU	P35406 carassius a
22	543.5	23.7	418	BIAR_MACMU	Q28524 macaca mula
23	539.5	23.5	398	BIAR_FELCA	Q91C64 felis silve
24	538.5	23.5	446	DADR_PIG	P50130 sus scrofa
25	538	23.5	386	DADR_OREMO	P47800 oreochromis
26	535.5	23.4	428	B4AR_MEIGA	P43141 meleagris g
27	533.5	23.3	446	DADR_RAT	P18901 rattus norv
28	531	23.2	408	BIAR_HUMAN	P13945 homo sapien
29	530.5	23.1	446	DADR_DIDMA	P42288 didelphis m
30	528.5	23.1	463	D5DR_FUGRU	P53454 fuigu rubrip
31	526.5	23.0	483	BIAR_MEIGA	P07700 meleagris g
32	524.5	22.9	459	D1DR_FUGRU	P53452 fuigu rubrip
33	524	22.9	351	B3AR_CAVPO	P60483 cavia porce

34	516	22.5	511	1	D0PL_DROME	P41596 drosophila
35	512.5	22.4	576	1	AIAD_RABIT	O02666 oryctolagus
36	508	22.2	379	1	AIAD_BALAM	Q93127 balanus amp
37	505.5	22.1	562	1	AIAD_MOUSE	P97714 mus musculu
38	504	22.0	451	1	DADR_XENLA	P42289 xenopus lae
39	503.5	22.0	561	1	DADR_RAT	P23944 rattus norv
40	503	21.9	572	1	AIAD_HUMAN	P25100 homo sapien
41	492.5	21.5	457	1	ABDR_XENLA	P42290 xenopus lae
42	492.5	21.5	539	1	D0P2_DROME	Q24563 drosophila
43	490.5	21.4	385	1	BIAR_XENLA	Q42574 xenopus lae
44	490.5	21.4	477	1	OAR_HELVI	Q25188 heliobius v
45	489.5	21.4	477	1	DBDR_HUMAN	P21918 homo sapien

## ALIGNMENTS

```

RESULT 1
ID      5H6_HUMAN          STANDARD:      PRT:      440 AA.
AC      P50406; Q13640;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      20-AUG-2001 (Rel. 40, Last annotation update)
DE      5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR).
GN      HTR6.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Striatum;
RX      MEDLINE=96102917; PubMed=8522988;
RA      Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
RT      Sibley D.R., Roth B., Hamblin M.W.;
RT      "Cloning, characterization, and chromosomal localization of a human
RL      5-HT6 serotonin receptor.";
RN      J. Neurochem. 66:47-56(1996).
RN      [2]
RP      SEQUENCE OF 215-280 FROM N.A.
RC      TISSUE=Striatum;
RX      MEDLINE=95385798; PubMed=7656980;
RA      Ulmer C., Schmuck K., Kalkman H.O., Lubbert H.;
RT      "Expression of serotonin receptor mRNAs in blood vessels.";
RN      FEBS Lett. 370:215-221(1995).
CC      -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
CC      5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION
CC      AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC      THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC      CYCLASE. IT HAS A HIGH AFFINITY FOR TRICICLIC PSYCHOTROPIC DRUGS.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN SEVERAL HUMAN BRAIN REGIONS. MOST
CC      PROMINENTLY IN THE CAUDATE NUCLEUS.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
EMBL: L41147; AAA92622.1; -
EMBL: 249119; CAA88929.1; -
DR      GCRDB: GCR_1062; -
DR      GCRDB: GCR_1885; -
DR      MIM: 601109; -
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR01102; 5HT6RECEPTR.
DR      PROSITE: PS00237; G_PROTEIN_RECEPTOR_1; 1.

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DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;  
 FT Multigene family.  
 FT DOMAIN 1 34  
 FT TRANSMEM 35 57  
 FT TRANSMEM 58 64  
 FT TRANSMEM 65 85  
 FT TRANSMEM 86 100  
 FT TRANSMEM 101 122  
 FT TRANSMEM 123 144  
 FT TRANSMEM 145 166  
 FT TRANSMEM 167 184  
 FT TRANSMEM 185 208  
 FT TRANSMEM 209 265  
 FT TRANSMEM 266 290  
 FT TRANSMEM 291 295  
 FT TRANSMEM 320 320  
 FT DOMAIN 321 440  
 FT DISULFID 99 180  
 FT CONFLICT 247 247  
 FT SEQUENCE 440 AA; 46954 MW; C888F47650C1D2EF CRC64;

Query Match 99.8%; Score 2287; DB 1; Length 440;  
 Best Local Similarity 99.8%; Pred. No. 5.4e-137;  
 Matches 439; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYPEPPTANSTPAMGAPSPAGSGWVAALCVIYALTAANSLLIALICTOPALRNT 60  
 DB 1 MYPEPPTANSTPAMGAPSPAGSGWVAALCVIYALTAANSLLIALICTOPALRNT 60  
 QY 61 SNFELVSLFTSDLMVGLVYVPPAMLNALYGRVNLARGICLMTAFDVMCCSASILNLCI 120  
 DB 61 SNFELVSLFTSDLMVGLVYVPPAMLNALYGRVNLARGICLMTAFDVMCCSASILNLCI 120  
 QY 121 SIDRYLLISPLRYKLRMTPLRALALVLGWSIALASFLPLLGLMHELGHARRPVPGQC 180  
 DB 121 SIDRYLLISPLRYKLRMTPLRALALVLGWSIALASFLPLLGLMHELGHARRPVPGQC 180  
 QY 121 SIDRYLLISPLRYKLRMTPLRALALVLGWSIALASFLPLLGLMHELGHARRPVPGQC 180  
 DB 181 RLILASLPVLAASGLTFPLPSGALICFTYCRILLAAKROAVOVSLLTGMASQASELLOYV 240  
 QY 181 RLILASLPVLAASGLTFPLPSGALICFTYCRILLAAKROAVOVSLLTGMASQASELLOYV 240  
 DB 181 RLILASLPVLAASGLTFPLPSGALICFTYCRILLAAKROAVOVSLLTGMASQASELLOYV 240  
 QY 241 RPPRPVESADSRRLATKHSRKALKAKLTGLIGMFEFTWLPFFVANIYQAVDCISFG 300  
 DB 241 RPPRPVESADSRRLATKHSRKALKAKLTGLIGMFEFTWLPFFVANIYQAVDCISFG 300  
 QY 301 LRDVLTWLGVCNSTMPITYPFMRDFKRALGFLPCPCPREKQASLASPSLRTSHSGP 360  
 DB 301 LRDVLTWLGVCNSTMPITYPFMRDFKRALGFLPCPCPREKQASLASPSLRTSHSGP 360  
 QY 361 RPLGLSLQOVLPLPPDDSDSDAGSGSSGLRLTAQLLPGANODPPLPTRAANAANVF 420  
 DB 361 RPLGLSLQOVLPLPPDDSDSDAGSGSSGLRLTAQLLPGANODPPLPTRAANAANVF 420  
 QY 421 FNIDPAEPELRPHPLGIPTN 440  
 DB 421 FNIDPAEPELRPHPLGIPTN 440

RESULT 2  
 5H6\_MOUSE  
 ID 5H6\_MOUSE STANDARD; PRT; 440 AA.  
 AC O9R1C8;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR).  
 GN HTR6  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Brain;  
 RA Kohen R., Guthrie C.R., Heidmann D.E.A., Hamblin M.W.;  
 RT "Mutagenesis studies of the mouse 5-HT6 serotonin receptor."  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 CC  
 CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-  
 CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS  
 CC A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS  
 CC RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE  
 CC CYCLASE. IT HAS A HIGH AFFINITY FOR TRICICLIC PSYCHOTROPIC DRUGS  
 CC (BY SIMILARITY).  
 CC  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: AF134158; AAD46490.1; -  
 DR MGD; MGI:1196627; Htr6.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;  
 FT Multigene family.  
 FT DOMAIN 1 34  
 FT TRANSMEM 35 57  
 FT TRANSMEM 58 64  
 FT TRANSMEM 65 85  
 FT TRANSMEM 86 100  
 FT TRANSMEM 101 122  
 FT TRANSMEM 123 144  
 FT TRANSMEM 145 166  
 FT TRANSMEM 167 184  
 FT TRANSMEM 185 208  
 FT TRANSMEM 209 267  
 FT TRANSMEM 268 292  
 FT TRANSMEM 293 297  
 FT TRANSMEM 328 322  
 FT TRANSMEM 323 440  
 FT DISULFID 99 180  
 FT CARBOHYD 9 9  
 FT SEQUENCE 440 AA; 46998 MW; 4440CDBE01FEF0C CRC64;

Query Match 86.8%; Score 1989; DB 1; Length 440;  
 Best Local Similarity 87.6%; Pred. No. 2.7e-118;  
 Matches 387; Conservative 15; Mismatches 36; Indels 4; Gaps 2;

QY 1 MYPEPPTANSTPAMGAPSPAGSGWVAALCVIYALTAANSLLIALICTOPALRNT 60  
 DB 1 MYPEPPTANSTPAMGAPSPAGSGWVAALCVIYALTAANSLLIALICTOPALRNT 60  
 QY 61 SNFELVSLFTSDLMVGLVYVPPAMLNALYGRVNLARGICLMTAFDVMCCSASILNLCI 120  
 DB 61 SNFELVSLFTSDLMVGLVYVPPAMLNALYGRVNLARGICLMTAFDVMCCSASILNLCI 120  
 QY 121 SIDRYLLISPLRYKLRMTPLRALALVLGWSIALASFLPLLGLMHELGHARRPVPGQC 180  
 DB 121 SIDRYLLISPLRYKLRMTPLRALALVLGWSIALASFLPLLGLMHELGHARRPVPGQC 180  
 QY 121 SIDRYLLISPLRYKLRMTPLRALALVLGWSIALASFLPLLGLMHELGHARRPVPGQC 180  
 DB 121 SIDRYLLISPLRYKLRMTPLRALALVLGWSIALASFLPLLGLMHELGHARRPVPGQC 180  
 QY 181 RLILASLPVLAASGLTFPLPSGALICFTYCRILLAAKROAVOVSLLTGMASQASELLOYV 240  
 DB 181 RLILASLPVLAASGLTFPLPSGALICFTYCRILLAAKROAVOVSLLTGMASQASELLOYV 240  
 QY 239 VPPRPVESADSRRLATKHSRKALKAKLTGLIGMFEFTWLPFFVANIYQAVDCIS 298  
 DB 239 VPPRPVESADSRRLATKHSRKALKAKLTGLIGMFEFTWLPFFVANIYQAVDCIS 298

Db 241 VPRTPPGMESADSRRLTKHSHKALKASLTLLGILSMFEVTLPEFVASIAQAVDCIS 300  
 QY 299 PGFEDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRGREOASLASLSTSHS 358  
 Db 301 PGFEDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRGREOASLASLSTSHS 360  
 QY 359 GPRPGSLDQOVLPLPPPSDSDSGSGSGLRLTAQLLPGCATODPPLTRAAAV 418  
 Db 361 GARGSLDQOVLPLPPPSDSDS--ASGGSGLQLLAQLLPGCATODPPLTRAAAV 418  
 QY 419 NFEVDPAPELRLPHLGIPTN 440  
 Db 419 NFEVTDVSEPEIRQHPLGSPMN 440  
 RESULT 3  
 SH6\_RAT STANDARD; PRT: 436 AA.  
 AC P31388;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DT 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR)  
 DE (ST-B17).  
 GN HTR6.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Striatum;  
 RX MEDLINE=93196608; PubMed=7680751;  
 RA Monsma F.J. Jr., Shen Y., Ward R.P., Hamblin M.W., Sibley D.R.;  
 RT Cloning and expression of a novel serotonin receptor with high  
 RL affinity for tricyclic psychotropic drugs.";  
 RL Mol. Pharmacol. 43:320-327(1993).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93277562; PubMed=8389146;  
 RA Ruat M., Traifort E., Ariang J.-M., Tardivel-Lacombe J., Diaz J.,  
 RA Leurs R., Schwartz J.-C.;  
 RT "A novel rat serotonin (5-HT6) receptor: molecular cloning,  
 RL localization and stimulation of cAMP accumulation.";  
 RL Biochem. Biophys. Res. Commun. 193:268-276(1993).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar;  
 RA Martial R.;  
 RT Submitted (xxx-1993) to the EMBL/Genbank/DBJ databases.  
 RL -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR  
 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION  
 AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF  
 THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE  
 CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS.  
 Db 181 RLASLPFVLVAGSLFFFLPSGAICFTYCRILLAARKQAVASLTGTGASQSEFLQVP 240  
 Db 181 RLASLPFVLVAGSLFFFLPSGAICFTYCRILLAARKQAVASLTGTGASQSEFLQVP 240  
 QY 241 RTRPGVGSADSRRLTKHSHKALKASLTLLGILSMFEVTLPEFVASIAQAVDCIS 300  
 Db 241 RTRPGVGSADSRRLTKHSHKALKASLTLLGILSMFEVTLPEFVASIAQAVDCIS 300  
 QY 301 LFDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRGREOASLASLSTSHS 351  
 Db 301 LFDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRGREOASLASLSTSHS 351  
 RESULT 4  
 B1AR\_MOUSE STANDARD; PRT: 466 AA.  
 AC P34971;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE BETA-1 ADRENERGIC RECEPTOR.

DR GCRDB: GCR\_0719;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm.1.1  
 DR PRINTS: PRO00237; GPCRHOOPS.  
 DR PRINTS: PRO1102; 5HTRECEPT.  
 DR PROSITE: PS00237; G\_PROTEIN\_REC\_P1.1;  
 DR PROSITE: PS00262; G\_PROTEIN\_REC\_P1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family.  
 FT DOMAIN 1 34  
 FT TRANSMEM 35 57  
 FT DOMAIN 58 64  
 FT TRANSMEM 65 85  
 FT DOMAIN 86 100  
 FT TRANSMEM 101 122  
 FT DOMAIN 123 144  
 FT TRANSMEM 145 166  
 FT DOMAIN 167 184  
 FT TRANSMEM 185 208  
 FT DOMAIN 209 265  
 FT TRANSMEM 266 290  
 FT DOMAIN 291 320  
 FT TRANSMEM 321 436  
 FT CARBOHYD 9 9  
 FT DISULFID 99 180  
 FT CONFLICT 57 57  
 FT CONFLICT 336 436  
 SQ SEQUENCE 436 AA; 46922 MW; 6BC00F6A3CBAB5FB4 CRC64;  
 Query Match 73.2%; Score 1678; DB 1; Length 436;  
 Best Local Similarity 91.7%; Pred. No. 9, 1e-99;  
 Matches 322; Conservative 6; Mismatches 23; Indels 0; Gaps 0;  
 QY 1 MYPEPGTANSTPWAGCAPSPAGSGWAAALCVYIALTAANSLILALICTOPALRNT 60  
 Db 1 MYPEPGTANSTPWAGCAPSPAGSGWAAALCVYIALTAANSLILALICTOPALRNT 60  
 QY 61 SNFEVLSLFTSDLMVGLVWPPAMLAALYGRWLAARGLCLMTAFVDFMCSSATLNLCL 120  
 Db 61 SNFEVLSLFTSDLMVGLVWPPAMLAALYGRWLAARGLCLMTAFVDFMCSSATLNLCL 120  
 QY 121 SLDRYLLIISPLRYKRLMTEPLRALALAVLGWASLAALASFLPLLGHELGHAHPVPGQC 180  
 Db 121 SLDRYLLIISPLRYKRLMTEPLRALALAVLGWASLAALASFLPLLGHELGHAHPVPGQC 180  
 QY 181 RLASLPFVLVAGSLFFFLPSGAICFTYCRILLAARKQAVASLTGTGASQSEFLQVP 240  
 Db 181 RLASLPFVLVAGSLFFFLPSGAICFTYCRILLAARKQAVASLTGTGASQSEFLQVP 240  
 QY 241 RTRPGVGSADSRRLTKHSHKALKASLTLLGILSMFEVTLPEFVASIAQAVDCIS 300  
 Db 241 RTRPGVGSADSRRLTKHSHKALKASLTLLGILSMFEVTLPEFVASIAQAVDCIS 300  
 QY 301 LFDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRGREOASLASLSTSHS 351  
 Db 301 LFDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRGREOASLASLSTSHS 351  
 RESULT 4  
 B1AR\_MOUSE STANDARD; PRT: 466 AA.  
 AC P34971;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE BETA-1 ADRENERGIC RECEPTOR.

```

GN      ADRB1 OR ADRB1R.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/5V.
RX      MEDLINE=93372116; PubMed=8395893;
RA      Jasper J.R., Link R.E., Chruscinski A.J., Koblika B.K., Bernstein D.;
RT      "Primary structure of the mouse beta 1-adrenergic receptor gene.";
RL      Biochim. Biophys. Acta 1178:307-309(1993).
CC      -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC      INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC      PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
CC      APPROXIMATIVELY EQUAL AFFINITY.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC      PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sdb.ch).
CC      -----
DR      EMBL, L10084; AAA02929.1; -.
DR      PIR, S36794; S36794.
DR      HSSP, P07700; IDEP.
DR      GCRDB: GCR_0578; -.
DR      MGD: MGI:87937; Adrb1.
DR      InterPro: IPR00276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCRHDOPSN.
DR      PRINTS: PR00561; ADRENERGICBLAR.
DR      PRINTS: PR01103; ADRENERGICR.
DR      PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR      PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein;
KW      Multi-pass type I; phosphorylation; lipoprotein; Palmitate.
FT      DOMAIN 1 59
FT      TRANSMEM 60 83
FT      DOMAIN 84 96
FT      TRANSMEM 97 120
FT      DOMAIN 121 131
FT      TRANSMEM 132 155
FT      DOMAIN 156 175
FT      TRANSMEM 176 199
FT      DOMAIN 200 221
FT      TRANSMEM 222 245
FT      DOMAIN 246 314
FT      TRANSMEM 315 338
FT      DOMAIN 339 345
FT      TRANSMEM 346 369
FT      DOMAIN 370 466
FT      CARBOHD 15 15
FT      DISULFD 131 209
FT      LIPID 381 381
FT      MOD_RES 296 296
FT      MOD_RES 301 301
FT      MOD_RES 401 401
FT      SEQUENCE 466 AA; 50479 MW; 753CD4C42BC9211 CRC64;

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Query Match	25.8%	Score 591.5	DB 1	Length 466
Best Local Similarity	35.9%	Pred. No. 1.6e-30		
Matches 158: Conservative	63	Mismatches 154	Indels 65	Gaps 17
QY	7	PTANSTPAMGAGPPAPAPGSGCWAA--ALCVVILTAANSLTALITCTOPALRRTSNF	63	
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Db      38  PASASLPPASES--SAPSLQQMTAGMGLLVALLVLLVIVGAVNVLVAIAKTPRLQTLNL 95
QY      64  ELVSLFTSDLMAGLVYMPRPAMINALYGNWVLARGCLLMTFEDVMCCSASLNLCLISLD 123
Db      96  FIMSLASADLVGLLIVLPEFGATIVYMGWMEYSEFCELMSTVDVLCTASLETCLTIALD 155
QY      124  RYLLLSLPLRYKLRMTPLRALATLVLGARSLAALASFLPILLGW--HELGNARPPV--PGQ 179
Db      156  RLATLTSPPRQSLTLTRARALVCTVAIALVSLPLILMHMRALSDERARCYNDPKC 215
QY      180  CRLLASLDFVLVAGLTFEFLPSGALICFTYCRILLARKOAVQAS----LTTGMSAQS-- 234
Db      216  CDFVTRRAYALASVVSSEYVELCIAMAFYLVTFPREDQOYKKIDSCERRFLGGARPSP 275
QY      235  EFLQYPRTPRGVESADSR-----RLATHSKKALKAKITLIGLGMFPVYVLPFEVA 287
Db      276  EFSPEPGRPPRLDLSIANGRSSKRRPSRLVALREBKALK--TLGIIMGVFLTCLMLPEFLA 332
QY      288  NIVQAV--CDICISPGLEFDVLTMGLYCNSTMPNDIY---PLEFKDRKRALGRFLPCPR--C 340
Db      333  NVKAFHFRDVLPRDLRFVEFMNLGANSFNFIICRSP----DPRKAFQHLCCARRAAC 368
QY      341  PRERQASLASPSLKTSHSGPPGIS--LQOVLPLPLP--PDSUSDSDAG----- 385
Db      389  RR-----RAAH--GDRPRPASGLARAGPPSPGASDDDDDDAGTTPPARLLEPW 436
QY      386  ---SGGSGLRLTAOLLPLG 402
Db      437  TGCGNGITTVDSDSLDEPG 456

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RESULT      5
BIAR_CANPA ID      BIAR_CANPA STANDARD; PRT; 473 AA.
AC      P79148;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      BETA-1 ADRENERGIC RECEPTOR.
GN      ADRB1.
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97364078; PubMed=9220370;
RA      Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascleri M.A.,
RT      Fong T.M.;
RT      "Molecular cloning of the dog beta 1 and beta 2 adrenergic
RT      receptors.";
RL      J. Recept. Signal Transduct. Res. 17:599-607(1997).
CC      -1- INDUCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC      INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC      PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NORPINEPHRINE WITH
CC      APPROXIMATELY EQUAL AFFINITY.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- PTM: HOMODOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC      PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
CC      SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U73207; AAB93648.1; -.
DR      HSSP; P07700; IDEP.
DR      GCRDB; GCR_1183; -.

```



DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PRO00237; GPCR\_RHODOPSIN.  
 DR PRINTS: PRO0561; ADRENRCGBLAR.  
 DR PRINTS: PRO1103; ADRENRCGBLAR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSMEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSMEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSMEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSMEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSMEM 222 245  
 FT TRANSMEM 246 322  
 FT TRANSMEM 323 346  
 FT TRANSMEM 347 353  
 FT TRANSMEM 354 377  
 FT DOMAIN 378 473  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT MOD\_RES 309 309  
 FT LIPID 389 389  
 SQ SEQUENCE 473 AA: 50060 MW: 361357 F7DF9DBD7E CRC64;

Query Match 25.6%; Score 587.5; DB 1; Length 473;  
 Best Local Similarity 35.6%; Pred. No. 2.8e-30;

Matches 160; Conservative 67; Mismatches 152; Indels 71; Gaps 19;

QY 1 MWPEGPSTANSTPMAGGPPSAPAGSGGWAA---ALCVIALTAANSLILALICTQPAL 57  
 DB 33 LVP-ASPSASPLAPTSSEGP--APLSQWTFAGIGLIMALLIVLLVAGNVLIAMIAIATPRL 89  
 QY 58 RMTSNFELWLSLSDMLVGLVMPAMLAALYGRWLVGLGLCLMTAFVYCCSASILNL 117  
 DB 90 QVLTNLFIMSLASADLVWGLVVPFGATVYMRGWEYSGFLCELTWSVDVLCVTASIEYL 149  
 QY 118 CUISTDRLYLILSLPKRYKRLMTPLRALATVLGWSLAALASFLPLLGLMHELG--HARPP 175  
 DB 150 CYTALDRYLAITAFPRYQSLTRARARALVCYMAISALVSEPLITLMMHWRAGGDARRC 209  
 QY 176 V--PGQCRLIASLPVLVASGLTFELPSGALCTCYCRILLAKRAQVOVAS---LTGM 229  
 DB 210 YNDPKCDEVTRNRAVAIASSVSEYVPLCMAFVLYLVFREAOQVKKIDSCERRFLGSP 269  
 QY 230 A-----SQASETLOVPTPRGVSS--ADSR-----RLATKRSKRALAKKLTGLL 273  
 DB 270 ARPPAPPPAPAPAPPPAPSPRAAALPANGVGRRRSPRLALREQALK--RLGII 326  
 QY 274 LGMEFTWMLPEFVAVIVQAV--CDCISPLGLFVYTLWGLYCSNPNPITY---PLFMDFKR 329  
 DB 327 MGVFTLCMLPEFLANVYKAFHRDLVPRDLFVFPNMLGYANSANFPLITTCRSP---DFKR 382  
 QY 330 ALGRFLPCPRCPREQASLASPSLRTSH--SGRPGLSLQOVLPLPLP-----PDSDDSDS 382  
 DB 383 AFQRLLCAR-----RAARGSHGACGDP-----RARPPSPCAASDDDDDDDD 426  
 QY 383 DAGSGSSGLRLTAQLLP-----GEATOD 407  
 DB 427 DAGAG--AGAAPPARLLLEPWAGCGGAAD 454

RESULT 6  
 BLAR\_RAT STANDARD; PRT: 466 AA.  
 AC P18090;  
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE BETA-1 ADRENERGIC RECEPTOR.  
 GN ADRB1 OR ADRB1R.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90350633; PubMed=1695899;  
 RA Machida C.A., Bunzow J.R., Searles R.P., van Tol H.H.M., Tepler B.,  
 RT Neve K.A., Teal P., Nipper V., Civelli O.;  
 RT "Molecular cloning and expression of the rat beta 1-adrenergic  
 RT receptor gene.";  
 RL J. Biol. Chem. 265:12960-12965(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90356399; PubMed=2167473;  
 RA Shimomura H., Terada A.;  
 RT "Primary structure of the rat beta-1 adrenergic receptor gene";  
 RL Nucleic Acids Res. 18:4591-4591(1990).  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 CC APPROXIMATELY EQUAL AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: J05561; AAA0792.1; -  
 DR EMBL: D00634; BAA00527.1; -  
 DR PIR: A36618; A36618.  
 DR PIR: S12591; S12591.  
 DR HSSP: P07700; IDEP.  
 DR GCRDB: GCR\_0126; -  
 DR GCRDB: GCR\_0127; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PRO00237; GPCR\_RHODOPSIN.  
 DR PRINTS: PRO0561; ADRENRCGBLAR.  
 DR PRINTS: PRO1103; ADRENRCGBLAR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSMEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSMEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSMEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSMEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSMEM 222 245  
 FT DOMAIN 246 314  
 FT TRANSMEM 315 338  
 FT DOMAIN 339 345  
 FT TRANSMEM 346 369  
 FT DOMAIN 370 466  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT LIPID 381 381

FT MOD\_RES 296 296 PHOSPHORYLATION (BY CARK) (POTENTIAL).  
 FT MOD\_RES 301 301 PHOSPHORYLATION (BY CARK) (POTENTIAL).  
 FT MOD\_RES 401 401 PHOSPHORYLATION (BY CARK) (POTENTIAL).  
 FT CONFLICT 162 162 L -> S (IN REF. 2).  
 FT CONFLICT 267 267 T -> S (IN REF. 2).  
 SQ SEQUENCE 466 AA; 50471 MW; 2955CB024944A12B CRC64;

Query Match 25.6%; Score 586.5; DB 1; Length 466;  
 Best Local Similarity 35.5%; Pred. No. 3; 2e-30;  
 Matches 156; Conservative 63; Mismatches 156; Indels 65; Gaps 16;

QY 7 PTANSPWAGCPSPAPGSGGWAA--ALCVVIALTAANSLLIALICQPALRINSF 63  
 DB 38 PPSALPAPASEG--SAPLSQMTAGMGLLALLVLLVGNVLYIAIAKTPRLQTLTNL 95  
 QY 64 FLVSLFTSDMLVGLVMPAMALYGRVYLAGLCLMTAFDVCMCCSASILNLCISLD 123  
 DB 96 FIMSLASADLVMLVLPFGATIVMGWMEYGSFCELMTSVDVLCVTASIEFLVIALD 155  
 DB 124 RYLLIISPLRYKLRMPRLRLALVLCANSLAALASFLPLILGW--HELGHARPPV--PGQ 179  
 DB 156 RYLAITLPRYOSLLTRARARALVCTVMAISALVSLPLIMHWRABESDEARCYNDPKC 215  
 QY 180 CRLLASLPVLYVAGLTFELPSGALCYCRILLARKOAVOAS-----LTGMSASQAS 234  
 DB 216 CPEVTRAAVAIASVSVFYPLICIMAFVILVREAKOKKIDSCERREFLGPPPPSP 275  
 QY 235 ETLQVPRTPRGVESADSR-----RLATKSRKALKAKLGLLIGMFVYMLPEFVA 287  
 DB 276 AVSPSPGPRPADSLANGRSSKRPSRLVALRQKALK--TLGIMGVFTLCLWLPFLA 332  
 QY 288 NIVQAN--CCGISPLGFDVLWLYGYNSTAMPITY---PLFMRFKALGRFLCPR---C 340  
 DB 333 NVYKAPHRDLVDRLEVFENWGLYANSAPNPIIYCRSP---DFKRAFORLLCCARRAC 388  
 QY 341 PERQASLASPLRTSHSGSRPGLS--LQOVLPLPLP--PDSDSDDAG----- 385  
 DB 389 RR-----RAAH--GDRPRASGCLARAGPPSPGAPSDDDDDAAGATPPARILLEW 436  
 QY 386 ---SGSSGLRLTAQLLLPG 402  
 DB 437 AGCNGGTTVDSDSLDEPG 456

RESULT 7  
 BIAR\_FELCA STANDARD: PRT; 474 AA.  
 QY 20-AUG-2001 (Rel. 40; Created)  
 DB 20-AUG-2001 (Rel. 40; Last sequence update)  
 DE 20-AUG-2001 (Rel. 40; Last annotation update)  
 DE BETA-1 ADRENERGIC RECEPTOR.  
 GN ADRB1.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxId=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cully D.F., Tremml G., Zachwieja S.;  
 RT "Felis domesticus beta adrenergic receptor subtype 1.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 APPROXIMATELY EQUAL AFFINITY (BY SIMILARITY).  
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC - PM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY  
 SIMILARITY).  
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AF192344; AAF04303.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1.1.  
 DR PRINTS: PRO00237; GPCRHOOPS.  
 DR PRINTS: PRO0561; ADRENERGICBLAR.  
 DR PRINTS: PRO1103; ADRENERGICR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPE\_F1.1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECPE\_F1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSMEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSMEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSMEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSMEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSMEM 222 245  
 FT DOMAIN 246 321  
 FT TRANSMEM 322 345  
 FT DOMAIN 346 352  
 FT TRANSMEM 353 376  
 FT DOMAIN 377 474  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT MOD\_RES 308 388  
 FT LIPID 388  
 SQ SEQUENCE 474 AA; 50532 MW; 2FC97DE4CFB7C3F CRC64;

Query Match 24.9%; Score 571; DB 1; Length 474;  
 Best Local Similarity 34.7%; Pred. No. 3; 1e-29;  
 Matches 162; Conservative 66; Mismatches 167; Indels 72; Gaps 20;

QY 1 WYEPGPTANSPWAGCPSPAPGSGGWAA--ALCVVIALTAANSLLIALICQPAL 57  
 DB 33 LVP-ASPSASPLTPISSEGP--APLSQMTAGIGLMLALVLLVGNVLYIAIAKTPRL 89  
 QY 58 RMTSNFVLVSLFTSDMLVGLVMPAMALYGRVYLAGLCLMTAFDVCMCCSASILN 117  
 DB 90 QLTNLEFIMSLASADLVMLVLPFGATIVMGWMEYGSFCELMTSVDVLCVTASIEFL 149  
 QY 118 CLISDRYLLIISPLRYKLRMPRLRLALVLCANSLAALASFLPLILGW--HELGHARPP 175  
 DB 150 CVIALDRYLAISPRYOSLLTRARARALVCTVMAISALVSLPLIMHWRABESDEARRC 209  
 QY 176 V--PGCRLASLPVLYVAGLTFELPSGALCYCRILLARKOAVOAS---LTTGM 229  
 DB 210 YNDPKCCPEVTRAAVAIASVSVFYPLICIMAFVILVREAKOKKIDSCERREFLSGP 269  
 QY 230 ASOASETLQVPRTPRGVESADS-----RLATKSRKALKAKLGLL 273  
 DB 270 ARPPSPA-PAPGSPRPAATAAAAAAALPLANGRIKRRRPSRLVALREKALK---TLGIT 325  
 QY 274 LGMFVYMLPEFVAVIVAV--CDCISPLGFDVLWLYGYNSTAMPITY---PLFMRDPKR 329  
 DB 326 MGVFLCLWLPFLAVVAVAFHRDLVDRLEVFENWGLYANSAPNPIIYCRSP---DFRK 381  
 QY 330 ALGRFLPCPCPREREQASLASPLTSH--SGPRGLS--LQOVLPLPLP--PDSDS 382  
 DB 382 AFORLL---CFARRAA-----RGHAAAGDRPRASGCLPGRTPSPGASDEDODD 430  
 QY 383 DAGSGSSGLRLTAQLLPGEATQDPPLPTRAAAVNFNID-PAEP 428

DB 431 DVGAP-----PARLEPWACNG-----GAAADSDSLDEPGR 466

RESULT 8

BLAR\_MACMU STANDARD: PRT: 480 AA.

AC P47899;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE BETA-1 ADRENERGIC RECEPTOR.

GN ADRB1.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.

OC NCBI\_TaxID=9544;

OX [1]

RP SEQUENCE FROM N.A.

RT MEDLINE=95078456; PubMed=7987008;

RT "The rhesus macaque beta 1-adrenergic receptor gene: structure of the gene and comparison of the flanking sequences with the rat beta 1-adrenergic receptor gene.";

RT RT adrenergic receptor gene.";

RT RT DNA Seq. 4:231-241(1994).

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATIVELY EQUAL AFFINITY.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: X75540; CAA53228.1; -

DR HSSP: P07700; IDEP.

DR GCRDB: GCR\_1746; -

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCRHHODOPSN.

DR PRINTS: PR00561; ADRENERGICBLAR.

DR PRINTS: PR01103; ADRENERGICR.

DR PROSITE: PS00337; G\_PROTEIN\_RECP\_FL\_1; 1.

DR PROSITE: PS50262; G\_PROTEIN\_RECP\_FL\_2; 1.

DR G-protein coupled receptor; transmembrane; glycoprotein; MultiGene family; Phosphorylation; Lipoprotein; Palmitate.

KW MultiGene family; Phosphorylation; Lipoprotein; Palmitate.

FT TRANSMEM 1 59

FT TRANSMEM 60 83

FT TRANSMEM 84 96

FT TRANSMEM 97 120

FT TRANSMEM 121 131

FT TRANSMEM 132 155

FT TRANSMEM 156 175

FT TRANSMEM 176 199

FT TRANSMEM 200 221

FT TRANSMEM 222 245

FT TRANSMEM 246 328

FT TRANSMEM 329 352

FT TRANSMEM 353 359

FT TRANSMEM 360 383

FT TRANSMEM 384 480

FT CARBOHYD 15 15

FT CARBOHYD 15 15

FT DISULFID 131 209

FT MOD\_RES 315 315

PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT MOD\_RES 415 415 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT LIPID 395 395 PALMITATE (BY SIMILARITY).

SO SEQUENCE 480 AA: 51608 MW: 25018PA03128084 CRC64:

Query Match 24.6%; Score 563.5; DB 1; Length 180;

Best Local Similarity 34.5%; Pred. No. 9, 1e-29;

Matches 149; Conservative 62; Mismatches 166; Indels 55; Gaps 14;

QY 1 MWPEPPTANSTPAMGAGPSAPAGSGWAA---ALCVYIALTAANSLLIALICTOPAL 57

DB 33 LVP-ASPPASLPPASEGP--EPISQOWTAGMGLMALVLLVAAGNVIVIAIAKTPRL 89

QY 58 RMTSNFELVSLFSDMLWGLVWVPMALNAIVGRWLGLCLLWAFVPMCCSASILNW 117

DB 90 QLTLLFMSLASDVLWGLVVPFGATTVWGRWYGSFCEELWTSVVLCTVASTETL 149

QY 118 CLTSDRYLLISPLRYKRMTPPLRALALVLGMSIALASFLPLDGLW--HELGHARPP 175

DB 150 CVIALDRYLAITSPEFYQSLTRARARGLVCTYMAISALVSFLPLMHMWRASDEARRC 209

QY 176 V--PGCRLLASLPEVLYVAGSLTFELPSCAICFTYCRILLARKQAVQAS---LTGM 229

DB 210 YNDPKCDEVTNRAVAIASVSVFYPLCIMAFLVLRVEREAKQYKIDSCERRFLGCP 269

QY 230 ASQASET-----LQVPRPRGVESADS-----RLATKHSKRLAKK 267

DB 270 ARPPSPSPSPSPVPVAPPPGPPRAAAATTPVLYNGRAGKRSPRLVALRQAKLK-- 327

QY 268 LTLGLLGFVYTLPEFVANIQAQV--CDICSPGLFDVLTWLCYSTNMPITY--PLF 323

DB 328 -FLGIMGVFTLCWLPFLFANVKAHRELVPRLFEVFWLGLYANSAPNPIIYCRSP-- 384

QY 324 MDPFKALRFLPCPCPRERQASLASPSLRTHSHSPRGLSLQVLPPLP--PDSDSS 382

DB 385 --DFRNAFORLLCCARRAARRHAHAGDRPRASGLARPG-----PPSPGASDDDD 435

QY 383 DAGSGSSGLRL 394

DB 436 DDVVGATOPARL 447

RESULT 9

BLAR\_PIG STANDARD: PRT: 468 AA.

AC Q28998; Q46575;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUL-1998 (Rel. 38, Last annotation update)

DE BETA-1 ADRENERGIC RECEPTOR.

GN ADRB1.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OC NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RT MEDLINE=98318327; PubMed=9655595;

RT Cao H., Bigwell C.A., Williams S.K., Liang W., Mills S.E.;

RT "Nucleotide sequence of the coding region for the porcine beta1-adrenergic receptor gene.";

RT J. Anim. Sci. 76:1720-1721(1998).

RN [2]

RP SEQUENCE OF 101-468 FROM N.A.

RA TISSUE=Heart;

RC Mcneel R.L., Mersmann H.J.;

RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATIVELY EQUAL AFFINITY (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS

CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY  
 CC SIMILARITY). BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -1- SIMILARITY:-----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF042454; AAB97525.1; -  
 DR EMBL: U56425; AAC06330.1; -  
 DR HSSP: P07700; IDEP  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPSN.  
 DR PRINTS: PR00561; ADRENERGICBLAR.  
 DR PRINTS: PR01103; ADRENERGICBLAR.  
 DR PROSITE: PS00237; G-PROTEIN-RECEP\_FL\_1; 1.  
 DR PROSITE: PS0262; G-PROTEIN-RECEP\_FL\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 DR Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 DR TRANSMEM 1 59  
 DR DOMAIN 1 (POTENTIAL).  
 DR TRANSMEM 60 83  
 DR TRANSMEM 84 96  
 DR TRANSMEM 97 121  
 DR TRANSMEM 122 132  
 DR TRANSMEM 133 153  
 DR TRANSMEM 154 176  
 DR TRANSMEM 177 197  
 DR TRANSMEM 198 223  
 DR TRANSMEM 224 244  
 DR TRANSMEM 245 315  
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 DR TRANSMEM 930 943  
 DR TRANSMEM 944 957  
 DR TRANSMEM 958 971  
 DR TRANSMEM 972 985  
 DR TRANSMEM 986 999  
 DR TRANSMEM 1000 1013  
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DB 150 CVALDRLATSPFRQSLTLRARARALVCTWALSALVFLPIFOMWMDADAKSRC 209
OY 176 --VPGOCRLIASLPEVLVAGLTFPLPSGAICFTYTCRILLAAKQAVOVAS---LTTGM 229
DB 210 YNDPECCDFIINGVYAITSSVSFVPLCIMAFLVLFVREAKQVKKIDSCERRFLSGP 269
OY 230 ASQASELQVPRPRGVEASDR-----RLATKHSKALAKLTLGLLGMFFVTWL 282
DB 270 ARLPSRA-PSGPPPLPAATVYANGRANKRPPRLVALREQKAL--TLGITMGVFTLCWL 325
OY 283 PEFVANIYOVAV-CDICISPGLEFVLTWLGVCNSTMNPITY---PLEMRDFKALGRFLPCP 338
DB 326 PEFLLAVVAFHHDVLDVDRLEFVFNMLGVANSAFNPIITGRSP-----DFKAKQRLCCCA 381
OY 339 RCRCRQASLASPLRTSHSGPPGSLQGVLPPLPPSDSDSAGSGSSGLRLTAQL 398
DB 382 R-----RAACGSHAAAGPPRALCLAVARPSFGAASDDDDDDDDDDVGAAPPVRL 434
399 LLP-----GEATQDDPLPTRAAAA 417
435 LEPWAGYNGGAANSSSDSPERSRACCA 462

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## RESULT 12

BLAR HUMAN STANDARD; PRT: 477 AA.

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AC P08588; 090K68; (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BETA-1 ADRENERGIC RECEPTOR.
GN ADRA1 OR ADRA1R OR BIAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OK NCBI_Taxid=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88068509; PubMed=2825170;
RA Friele T., Collins S., Daniel K.W., Caron M.G., Lefkowitz R.J.,
RA Koblika B.K.;
RT "Cloning of the cDNA for the human beta 1-adrenergic receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7920-7924(1987).
RN 12
RX VARIANT ARG-389.
RX MEDLINE=99230291; PubMed=10212248;
RA Mason D.A., Moore J.D., Green S.A., Liggett S.B.;
RT "A gain-of-function polymorphism in a G-protein coupling domain of the
RT human beta1-adrenergic receptor.";
RL Hum. Mutat. 14:271-271(1999).
RN 13
RX VARIANTS GLY-49 AND ARG-389.
RX MEDLINE=99407229; PubMed=10477438;
RA Moore J.D., Mason D.A., Green S.A., Hsu J., Liggett S.B.;
RT "Racial differences in the frequencies of cardiac beta(1)-adrenergic
RT receptor polymorphisms: analysis of c145A>G and c1165G>C.";
RL Hum. Mutat. 14:271-271(1999).
RN 14
RX VARIANT GLY-49.
RX MEDLINE=20507547; PubMed=11052857;
RA Borjesson M., Magnusson Y., Hjalmarson A., Andersson B.;
RT "A novel polymorphism in the gene coding for the beta(1)-adrenergic
RT receptor associated with survival in patients with heart failure.";
RL Eur. Heart J. 21:1853-1858(2000).
CC -I- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
CC APPROPRIATELY EQUAL AFFINITY.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- PTM: HOMODIOLUS DESENITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.

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CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03019; AA51667.1; -
DR EMBL: AF169006; AA53696.1; -
DR EMBL: AF169007; AA53697.1; -
DR PIR: A39911; A39911.
DR HSSP: P07700; IDEP.
DR GCRDB: GCR_0048; -
DR MIM: 109630; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PRINTS: PR00561; ADRENERGICAR.
DR PRINTS: PR01103; ADRENERGICR.
DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate;
KW Polymorphism.
FT DOMAIN 1 59
FT TRANSMEM 60 83
FT DOMAIN 84 96
FT TRANSMEM 97 120
FT DOMAIN 121 131
FT TRANSMEM 132 155
FT DOMAIN 156 175
FT TRANSMEM 176 199
FT DOMAIN 200 221
FT TRANSMEM 222 245
FT DOMAIN 246 325
FT TRANSMEM 326 349
FT DOMAIN 350 356
FT TRANSMEM 357 380
FT DOMAIN 381 477
FT CARBOHYD 15 15
FT DISULFID 131 209
FT MOD_RES 312 312
FT MOD_RES 412 412
FT LIPID 392 392
FT VARIANT 49 49
FT VARIANT 389 389
FT SEQUENCE 477 AA; 51223 MW; 1D15E6390B5364B8 CRC64;
SQ
Query Match 24.3%; Score 557; DB 1; Length 477;
Best Local Similarity 33.8%; Pred. No. 2.3e-28;
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;
OY 1 NVPEPGPTANSTPWAGAGPPAPGSGVAAALCVIALTAANSLTALICTOPALRNF 60
DB 33 LVPASPPASLPPASESEPPSLSQWNTAGGLMALIVLIVAGNVLYALAKTRLOTL 92
OY 61 SNFELVSLTSDLMVGLVMPAPMALNYGRVNLARGLCLMTADVMCCSASINLCIL 120
DB 93 TNLFTMSASDLVGLVPGATIVVGRWEYSFCEIEMTSVDLCVPASIEITLCVI 152
OY 121 SLDRLLTSLSPRYKRLMTPRALALVIGAMSLAASFLPILGW--HELGHAPPV-- 176
DB 133 ALDRLATSPRYOSLTLRARARGLVCTWALSALVFLPLTMHMAEESDEARCYND 212
OY 177 PGQCLLASLPEVLVAGLTFPLPSGAICFTYTCRILLAAKQAVOVAS---LTTGMA 232
DB 213 PKCCDFVNRVAVLASSVSFVPLCIMAFLVLFVREAKQVKKIDSCERRFLSGP 272

```



ID	NAME	STANDARD	PRT	AA
DB	364 REEHLAASPAPRAS			398
QY	387 GGSGCL 392			
DB	399 GASGCL 404			
RESULT 14				
ID	B3AR_SHEEP	STANDARD	PRT	405 AA.
AC	09XT58:			
DT	20-AUG-2001 (Rel. 40, Created)			
DT	20-AUG-2001 (Rel. 40, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	BETA-3 ADRENERGIC RECEPTOR.			
OS	ADRB3.			
OS	Ovis aries (Sheep).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
CC	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MERINO.			
RX	MEDLINE=20292453; PubMed=10834601;			
RA	Forrest R.H., Hickford J.G.H.;			
RT	"Rapid communication: nucleotide sequences of the bovine, caprine, and			
RL	ovine beta3-adrenergic receptor genes.";			
CC	J. Anim. Sci. 78:1397-1398(2000).			
CC	-1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-			
CC	INDUCED ACTIVATION OF ADENYLYL CYCLASE THROUGH THE ACTION OF G			
CC	PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND			
CC	THERMOGENESIS.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL, AF109928; AAD26147.1; -			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PRINTS; PR00563; ADRENERGCB3AR.			
DR	PRINTS; PR01103; ADRENERGICR.			
DR	PROSITE; PS00237; G-PROTEIN_RECCEP_F1.1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECCEP_F1.2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Glycoprotein;			
KW	Multiogene family; Phosphorylation; Lipoprotein; Palmitate.			
FT	DOMAIN 1 36			
FT	TRANSMEM 37 63			
FT	DOMAIN 64 72			
FT	TRANSMEM 73 91			
FT	DOMAIN 92 111			
FT	TRANSMEM 112 133			
FT	DOMAIN 134 155			
FT	TRANSMEM 156 178			
FT	DOMAIN 179 203			
FT	TRANSMEM 204 225			
FT	DOMAIN 226 292			
FT	TRANSMEM 293 314			
FT	DOMAIN 315 326			
FT	TRANSMEM 327 347			
FT	DOMAIN 348 405			
FT	CARBOHYD 8 26			
FT	CARBOHYD 26 8			
FT	DISULFID 110 189			

FT	LIPID	361	361	PALMITATE (BY SIMILARITY)
5Q	SEQUENCE	405 AA;	43032 MW;	A2BAANAABE798ADS CXC64;
	Query Match	24.1%;	Score 553.5;	DB 1; Length 405;
	Best Local Similarity	34.3%;	Pred. No. 3.3e-28;	
	Matches 144;	Conservative 56;	Mismatches 165;	Indels 55; Gaps 13;
QY	1	MVEPEG-PTANSTPMAGGPPSPGSGGMAALCVIALTPAANSILIALICQPALRN	59	
DB	11	LTPWEDITTLAPNTANASGLPCVPMAVALAGALLALAVATYGGNLVVALARTPILOT	70	
QY	60	TSNFEVLFTSDLMVGLVMPAPMALNLGYRMVLYARGCLMTAFDVMCCSASTLNLCL	119	
DB	71	MTNVEVSTLATADLVGLLVPPGATLALTGHWPLGVNGCELMTSVDVLCTVASIEFLCA	130	
QY	120	ISLDYVLLILSLRKLMPTLRALALVAGMSLAALASFLPDLIGNHELG-----H	171	
DB	131	LAVDYVLYVTPDLRGAIVLTKRRARAAYLVVWVSAVAFIMSKMRVGDADAEORCH	190	
QY	172	ARPPGCGCRLLASLPFLVAVAGLTFEFLPSGALICFTYCRILLAAKQAVOV-----	222	
DB	191	SNPRC---CTFASNMNPYALLSSVSFYLPVLMLFVYARVFPVDIROLRLRLRELGRRP	247	
QY	223	----ASLTGMAASQSETLOYPTPTPGVESADSR--RLATKHSKALKAKVLGILG	275	
DB	248	EESPAPRSQSPGAG-----PYASPGAVPSYGRRAPIRLPLREHRAIR--DLGLIMG	299	
QY	276	MEFVWLMFEFVANYVQAV--CDCISPGFEDVLTWYGNSNTNPITY---PLFMDPKRA	330	
DB	300	TFTLWLMFEFVANYVYRALGSPVSGPFTLALMWLGANSAPNPLITGRSP----DFRSA	355	
QY	331	LGRFLPCRCRPREROASIASPSLRTSHSGPRGSLQGVLPPLPDPDSDDSDAGSGSS	390	
DB	356	FRRLP-C-RCPPEEHLAASP-----PRAPSGAPVLTSPAPGRQPSPLDGASGLS	405	
RESULT 15				
BAR-MOUSE	3BAR-MOUSE	STANDARD;	PRT;	400 AA.
AC	P25962; Q9Q298;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	BETA-3 ADRENERGIC RECEPTOR.			
GN	ADRB3 OR ADRB3R OR B3BAR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SMISS;			
RX	MEDLINE=92037534; Pubmed=1718744;			
RA	Nahmias C., Blin N., Elalouf J.M., Mattei M.-G., Strosberg A.D.,			
RA	Emorine L.J.;			
RT	"Molecular characterization of the mouse beta 3-adrenergic receptor:			
RT	relationship with the atypical receptor of adipocytes.";			
RL	EMBO J. 10:3721-3727(1991).			
RN	[2]			
RP	REVIEWS; SEQUENCE FROM N.A.			
RX	MEDLINE=93279311; Pubmed=8389293;			
RA	van Sproonsen A., Nahmias C., Krief S., Briand-Sutren M.-M.,			
RA	Strosberg A.D., Emorine L.J.;			
RT	"The promoter and intron/exon structure of the human and mouse beta			
RT	3-adrenergic-receptor genes.";			
RL	Eur. J. Biochem. 213:1117-1124(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM B).			
RC	STRAIN=C57BL/6; TISSUE=Brown adipose tissue;			
RX	MEDLINE=99396494; Pubmed=10455305;			
RA	Evans B.A., Papaioannou M., Hamilton S., Summers R.J.;			
RT	"Alternative splicing generates two isoforms of the beta3-adrenoceptor			



RT which are differentially expressed in mouse tissues.;

RL Br. J. Pharmacol. 127:1525-1531(1999).

RN [4]

RP SEQUENCE OF 378-400 FROM N.A.

RC TISSUE-Adipose tissue;

RX MEDLINE=93125503; Pubmed=1336117;

RA Granneman J.G., Lehnerts K.N., Rao D.D.;

RT "Rodent and human beta 3-adrenergic receptor genes contain an intron within the protein-coding block.;"

RL Mol. Pharmacol. 42:964-970(1992).

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEIN. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND THERMOGENESIS.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM A (SHOWN HERE) AND ISOFORM B; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES, AND DIGESTIVE TRACT. ISOFORM B HIGHEST IN BRAIN.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: X72862; CAAS1384.1; -

DR EMBL: X60438; CAA42966.1; -

DR EMBL: AF193027; AAF05768.1; -

DR EMBL: S53290; AAB24836.1; -

DR PIR: S18548; S18548.

DR PIR: S32804; S32804.

DR HSSP: P07700; IDEP.

DR GCRDB: GCR\_0253; -

DR GCRDB: GCR\_0551; -

DR GCRDB: GCR\_0708; -

DR MGD: MGI:87939; Adrb3.

DR InterPro: IPR00276; GPCR\_Rhodopsin.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_RHODOPSIN.

DR PRINTS: PR00563; ADRENERGIC3AR.

DR PRINTS: PR01103; ADRENERGIC3AR.

DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.

DR PROSITE: PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate; Alternative splicing.

FT DOMAIN 1 36

FT TRANSMEM 37 60

FT DOMAIN 61 69

FT TRANSMEM 70 88

FT DOMAIN 89 108

FT TRANSMEM 109 130

FT DOMAIN 131 152

FT TRANSMEM 153 175

FT DOMAIN 176 200

FT TRANSMEM 201 222

FT TRANSMEM 223 289

FT DOMAIN 290 311

FT TRANSMEM 312 323

FT TRANSMEM 324 344

FT DOMAIN 345 400

FT CARBOHYD 8 400

FT CARBOHYD 26 26

FT DISULFID 107 186

FT LIPID 358 358

FT VARSPIC 388 400

SEQUENCE 400 AA: 43006 MW: 3745072C01DFA32E CRC64;

Query Match 24.1%; Score 552.5; DB 1; Length 400;

Best Local Similarity 35.1%; Pred. No. 3.8e-28;

Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

QY 5 PGPTANSTPA-WGAP---PSAPGSG-----WVAALCVIAL-TAANSLTALICTQ 54

Db 3 PMPHRNSLALMSDAPTLDPANANTSGLPVMAALAGALLATATGAGNLVIALIART 62

QY 55 PALNTSNFLVLSLFTSDLVGLVMPAMINALGRVITARGICLMTAFDWCCKSAKI 114

Db 63 PRLQITINVEFTSLAADLVVGLVMPGATLALTGMPLETCCELTMSVIVLCVTASI 122

QY 115 LNLCLISDRFLILPLRYKRLMTPLRALVILGANSIALASFLPLGLGHELG---- 170

Db 123 ETLALAVDRILAVTNPLRGITLVTKRRARAAYLVIVSAVSFAPLMSMMRVGADAE 182

QY 171 ---HARPPVPGCRLLASLPFLVAGSLPFLPSGAICTFYCRITLLARKQAVASLT 226

Db 183 AQECHSNPRC---CSFASNMRYALLSSVSFYLLVLMFYARVFAKRR--HLRRE 238

QY 227 TGMASQASETLQVTRTPP-----GVESADSR--RLATKSKKALKLTLGILL 274

Db 239 LGRSPESP 295

QY 275 GMFVTVLPFVANIYAVC--DCISGLPDLVTLGVCNSTMPITY---PLFMRPKR 329

Db 296 GIESLCWLPFLAVLALAGPSLVPSGVFIALNMLGTANSAPNPVYICNSPDRDFAFR 355

QY 330 AL---GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP 362

Db 356 LLCYGGGPEEPRAVTFPPASPVEARQSPPLNRDGVGEGARP 397

Search completed: March 15, 2002, 14:14:26

Job time: 211 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:08:55 ; Search time 17.53 Seconds  
(without alignments)  
1911.968 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292  
Sequence: 1 MVEPEPTANSTPAWGAGP.....FNIDPAPELRPHPLGPTN 440

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2387	99.8	430	2	JC5520
2	1899.5	82.9	437	2	J57942
3	1678	73.2	436	2	JN0591
4	591.5	25.8	466	2	S36794
5	581	25.3	464	2	S12591
6	563.5	24.6	480	2	I53053
7	557	24.3	477	1	ORHUB1
8	554	24.2	405	2	S65459
9	552.5	24.1	400	2	S32804
10	552.5	24.1	446	1	DYHND1
11	551.5	24.1	400	2	A41679
12	551.5	24.1	400	2	A53281
13	547.5	23.9	363	2	I50475
14	543.5	23.7	418	2	G02953
15	538.5	23.5	446	2	I47217
16	538	23.5	386	2	S72168
17	535.5	23.4	428	2	A55044
18	533.5	23.3	487	1	DYRDL
19	531	23.2	408	1	ORHUB2
20	531	23.2	414	1	ORHUB3
21	528.5	23.1	463	2	B56849
22	526.5	23.0	483	2	A25896
23	525	22.9	385	2	S68780
24	524.5	22.9	459	2	A56849
25	516	22.5	511	2	S44275
26	508	22.2	379	2	JC6178
27	507.5	22.1	560	2	A36731
28	504	22.0	451	2	I51659
29	503	21.9	572	2	I39369

30	500	21.8	450	2	A55886	dopamine receptor
31	499.5	21.8	501	2	JH0447	alpha-1A-adrenergic
32	492.5	21.5	457	2	I51660	dopamine D1B recep
33	489.5	21.4	477	1	DYHND5	dopamine receptor
34	487.5	21.3	444	2	C55886	dopamine receptor
35	487.5	21.3	475	2	A41271	dopamine receptor
36	487	21.2	465	2	I51661	dopamine D1C recep
37	487	21.2	515	2	JC1525	alpha-1B-adrenergic
38	486	21.2	515	2	A40491	alpha-1-adrenergic
39	482	21.0	359	2	A35008	histamine H2 recep
40	480.5	21.0	517	2	A45121	alpha-1B adrenergic
41	480	20.9	484	2	S58868	G protein-coupled
42	479.5	20.9	445	2	A48881	serotonin receptor
43	477	20.8	359	2	JH0449	histamine H2 recep
44	477	20.8	486	2	B55886	dopamine receptor
45	476.5	20.8	377	2	S68423	serotonin receptor

## ALIGNMENTS

RESULT 1  
JC5520  
serotonin receptor 6 - human  
N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)  
C:Species: Homo sapiens (man)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 05-Nov-1999  
C:Accession: JC5520  
J:Kohen, R.; Metcalfe, M.A.; Khan, N.; Druck, T.; Huebner, K.; Lachowicz, J.E.; Melzke  
R.; Neurochem. 66, 47-56, 1996  
A:Title: Cloning, characterization, and chromosomal localization of a human 5-HT 6 se  
A:Reference number: JC5520; MUID:96102917  
A:Accession: JC5520  
A:Molecule type: mRNA  
A:Residues: 1-440 <KOH>  
A:Cross-references: GB:I41147; NID:91162923; PIDN:AAA92622.1; PID:91162924  
A:Experimental source: brain  
C:Comment: This protein shows high affinity for several therapeutically important ant  
C:Genetics:  
A:Gene: HTR6  
A:Map position: 1p35-36  
A:Introns: 238/3; 291/3  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran  
F:28-51/Domain: transmembrane #status predicted <TM1>  
F:65-88/Domain: transmembrane #status predicted <TM2>  
F:100-123/Domain: transmembrane #status predicted <TM3>  
F:143-166/Domain: transmembrane #status predicted <TM4>  
F:185-208/Domain: transmembrane #status predicted <TM5>  
F:266-289/Domain: transmembrane #status predicted <TM6>  
F:298-321/Domain: transmembrane #status predicted <TM7>  
F:10/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 99.8%; Score 2287; DB 2; Length 440;

Best local similarity 99.8%; Pred. No. 8.6e-170;  
Matches 439; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MVEPEPTANSTPAWGAGPSPAGSGGWAALCVYIALTAANSLIALICIQPALRNT 60
DB	1	MVEPEPTANSTPAWGAGPSPAGSGGWAALCVYIALTAANSLIALICIQPALRNT 60
QY	61	SNFELVSLFTSDLMVGLVWPPAMLNALGRVWLAGLCLMTAFVVMCCSASILNCL 120
DB	61	SNFELVSLFTSDLMVGLVWPPAMLNALGRVWLAGLCLMTAFVVMCCSASILNCL 120
QY	121	SDRYLLIISPLRYKRLRMTPLRALATVLGAMSLAALASFLPLLIGWHELGSHARPVPGOC 180
DB	121	SDRYLLIISPLRYKRLRMTPLRALATVLGAMSLAALASFLPLLIGWHELGSHARPVPGOC 180
QY	181	RLIASLPVYLVASGLTFPEPSAICFTYCRILLANKQAVQVSLTTGMASSQSEFLQVP 240
DB	181	RLIASLPVYLVASGLTFPEPSAICFTYCRILLANKQAVQVSLTTGMASSQSEFLQVP 240

QY 241 RTRPGVESADSRRLATKHSRKALAKLTGLTGLMFEVTVLPFFVANIQAACDCISPG 300  
 |||||||  
 Db 241 RTRPGVESADSRRLATKHSRKALAKLTGLTGLMFEVTVLPFFVANIQAACDCISPG 300  
 QY 301 LFDVLTWLGVCNSTNNPIIYPLFMRDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360  
 |||||||  
 Db 301 LFDVLTWLGVCNSTNNPIIYPLFMRDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360  
 QY 361 RFGSLQOVLPPLPPDSDSDSAGSGSSGLRLTAOLLPEATODPLPRAAAVNF 420  
 |||||||  
 Db 361 RFGSLQOVLPPLPPDSDSDSAGSGSSGLRLTAOLLPEATODPLPRAAAVNF 420  
 QY 421 FNIDPAEELRPHPLGIPTN 440  
 |||||||  
 Db 421 FNIDPAEELRPHPLGIPTN 440

## RESULT 2

7942  
 C:hydroxytryptamine receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
 C:Accession: I57942  
 R:Monma, F.J.  
 Mol. Pharmacol. 43, 320-327, 1993  
 A:Title: Cloning and expression of a novel serotonin receptor with high affinity for tr  
 A:Reference number: I57942; MUID:93196608  
 A:Accession: I57942  
 A:Status: preliminary: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-437 <RES>  
 A:Cross-references: GB:L03202; NID:g294507; PIDN:AAA0618.1; PID:g294508  
 C:Superfamily: vertebrate rhodopsin

Query Match 82.9%; Score 1899.5; DB 2; Length 437;  
 Best Local Similarity 84.5%; Pred. No. 9e-140;  
 Matches 376; Conservative 11; Mismatches 145; Indels 13; Gaps 4;

QY 1 MYPEPGPTANSTPAGAGPPAPSGGWWAAALCVIALTAANSLTALICTOPALRNT 60  
 |||||||  
 Db 1 MYPEPGPTANSTPAGAGPPAPSGGWWAAALCVIALTAANSLTALICTOPALRNT 60  
 QY 61 SNFVLVSFTSDLMVGLVMPAMLNALYGRWVLAAGLCCLMTAFDVMCCSASILNLCII 120  
 |||||||  
 Db 61 SNFVLVSFTSDLMVGLVMPAMLNALYGRWVLAAGLCCLMTAFDVMCCSASILNLCII 120  
 QY 121 SLDRLVLTSLRYKLRMTAPRALALILGAWSLAALASFLPLLGWHELGKARTAPGQC 180  
 |||||||  
 Db 121 SLDRLVLTSLRYKLRMTAPRALALILGAWSLAALASFLPLLGWHELGKARTAPGQC 180  
 QY 181 RLASLPEVLVAGSLTFELPSGAICFTYCRILIAARKQAVQVASTTGMAASQASETLQVP 240  
 |||||||  
 Db 181 RLASLPEVLVAGSLTFELPSGAICFTYCRILIAARKQAVQVASTTGMAASQASETLQVP 240  
 QY 241 RTRPGVESADSRRLATKHSRKALAKLTGLTGLMFEVTVLPFFVANIQAACDCISPG 300  
 |||||||  
 Db 241 RTRPGVESADSRRLATKHSRKALAKLTGLTGLMFEVTVLPFFVANIQAACDCISPG 300  
 QY 301 LFDVLTWLGVCNSTNNPIIYPLFMRDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360  
 |||||||  
 Db 301 LFDVLTWLGVCNSTNNPIIYPLFMRDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360  
 QY 361 RFGSLQOVLPPLPPDSDSDSAGSGSSGLRLTAOLLPEATODPLPRAAAVNF 420  
 |||||||  
 Db 361 RFGSLQOVLPPLPPDSDSDSAGSGSSGLRLTAOLLPEATODPLPRAAAVNF 420  
 QY 421 FNIDPAEELRPHPLGIPTN 440  
 |||||||  
 Db 421 FNIDPAEELRPHPLGIPTN 440  
 QY 437 TVNFEVTVDSVEPEIRPHPLSPVN 437

## RESULT 3

JN0591  
 C:serotonin receptor 6 - rat  
 N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 05-Nov-1999  
 C:Accession: JN0591  
 R:Ruft, M.; Traiffort, E.; Arrang, J.M.; Tardivel-Lacombe, J.; Diaz, J.; Leurs, R.; S  
 Biochem. Biophys. Res. Commun. 193, 268-276, 1993  
 A:Title: A novel rat serotonin (5-HT6) receptor: molecular cloning, localization and  
 A:Reference number: JN0591; MUID:93277562  
 A:Accession: JN0591  
 A:Molecule type: DNA  
 A:Residues: 1-436 <RNA>  
 A:Cross-references: GB:S62043; NID:g385708; PIDN:AA026508.1; PID:g385709  
 C:Genetics:  
 A:Introns: 238/3  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein  
 F:29-53/Domain: transmembrane #status predicted <TM1>  
 F:63-84/Domain: transmembrane #status predicted <TM2>  
 F:95-122/Domain: transmembrane #status predicted <TM3>  
 F:141-168/Domain: transmembrane #status predicted <TM4>  
 F:185-213/Domain: transmembrane #status predicted <TM5>  
 F:267-293/Domain: transmembrane #status predicted <TM6>  
 F:297-319/Domain: transmembrane #status predicted <TM7>  
 F:9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.2%; Score 1678; DB 2; Length 436;  
 Best Local Similarity 91.7%; Pred. No. 1.3e-122;  
 Matches 322; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 1 MYPEPGPTANSTPAGAGPPAPSGGWWAAALCVIALTAANSLTALICTOPALRNT 60  
 |||||||  
 Db 1 MYPEPGPTANSTPAGAGPPAPSGGWWAAALCVIALTAANSLTALICTOPALRNT 60  
 QY 61 SNFVLVSFTSDLMVGLVMPAMLNALYGRWVLAAGLCCLMTAFDVMCCSASILNLCII 120  
 |||||||  
 Db 61 SNFVLVSFTSDLMVGLVMPAMLNALYGRWVLAAGLCCLMTAFDVMCCSASILNLCII 120  
 QY 121 SLDRLVLTSLRYKLRMTAPRALALILGAWSLAALASFLPLLGWHELGKARTAPGQC 180  
 |||||||  
 Db 121 SLDRLVLTSLRYKLRMTAPRALALILGAWSLAALASFLPLLGWHELGKARTAPGQC 180  
 QY 181 RLASLPEVLVAGSLTFELPSGAICFTYCRILIAARKQAVQVASTTGMAASQASETLQVP 240  
 |||||||  
 Db 181 RLASLPEVLVAGSLTFELPSGAICFTYCRILIAARKQAVQVASTTGMAASQASETLQVP 240  
 QY 241 RTRPGVESADSRRLATKHSRKALAKLTGLTGLMFEVTVLPFFVANIQAACDCISPG 300  
 |||||||  
 Db 241 RTRPGVESADSRRLATKHSRKALAKLTGLTGLMFEVTVLPFFVANIQAACDCISPG 300  
 QY 301 LFDVLTWLGVCNSTNNPIIYPLFMRDFKRALGRFLPCVHCPEHRPALPPP 351  
 |||||||  
 Db 301 LFDVLTWLGVCNSTNNPIIYPLFMRDFKRALGRFLPCVHCPEHRPALPPP 351

## RESULT 4

S36794  
 beta-1-adrenergic receptor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 09-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 13-Aug-1999  
 C:Accession: S36794  
 R:Jaeger, J.R.; Link, R.E.; Chruschinski, A.J.; Kobilka, B.K.; Bernstein, D.  
 Biochim. Biophys. Acta 1178, 307-309, 1993  
 A:Title: Primary structure of the mouse beta(1)-adrenergic receptor gene.  
 A:Reference number: S36794; MUID:93372116  
 A:Accession: S36794  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-466 <JAS>  
 A:Cross-references: EMBL:L10084; NID:g293278; PIDN:AAA02929.1; PID:g293279

Query Match	25.8%;	Score 591.5;	DB 2;	Length 466;
Best Local Similarity	35.9%;	Pred. NO. 2.1e-38;		
Matches 158;	Conservative 63;	Mismatches 154;	Indels 65;	Gaps 17

RESULT 5  
S12591  
beta-1-adrenergic receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Jun-2000  
C:Accession: S12591 \$A0185; A36518  
R:Shimomura, H.; Terada, A.  
Nucleic Acids Res. 18, 4591, 1990  
Title: Primary structure of the rat beta-1 adrenergic receptor gene.  
Reference number: S12591, PMID:9035698

Query Match	25.3%	Score 581	DB 2	Length 464
Best Local Similarity	35.5%	Pred. No. 1,46-37		
Matches 156	Conservative 63	Mismatches 155	Indels 66	Gaps 17
QY	7	PTANSTPAMGAGPPSAPGSGWVAA--ALCVIALTAANSLLALICTOPALRNTSNF	63	
Db	37	PPASILTPASEG--SAPISQOWTAGMGLLIALIVLVVGVVIVAIKTPRLQTLTNL	94	
QY	64	FLVSLFTSDLMWGVVMPMPALNLYGKRVYALRGCLLTWTFADVWCCSASITNL	123	
Db	95	FIMSLASADLMVGLLVPEGATIVWGRWEXGFEFLMTSDVLCVVASIETLCVILD	154	
QY	124	RYLLILSPRLKRYLNTPLRALALVGAWSLAALASFLLTLGW--HELGHKRPV--PQO	179	
Db	155	RYLAITSPFRQOSLITRARA--ALVCTVMAISALVSFLPLMHMMRAESEDARCRNDPKC	213	
QY	180	CRLLASLPEFLVLSAGLTFELPSGAICTYTCRILLAAKQAVQVSLTGMAS----	234	
Db	214	CDPFTNRAVYLAASSVSEFYVPLCINAFYLLVFREACKQVKKIDSCERRFLSGPRPSP	273	
QY	235	ETLQVPRPRGVESADSR-----RLATKHSRKALKAKLTLGLLGMFVYMLPEFVA	287	
Db	274	APSPGCPRRPADSLANRSKRRPSRLVALREQALK--TLGITKVFLLCPFEFLA	330	
QY	288	NIVQAV--CDCISPGLEFDLTLWGYCNSITMNPDIY--PLFMKDFKRALGRELPQPR--	340	
Db	331	NVKAHFHRLDVLPRDLFEVFNWLGVAANSFNPDIYCRSP--DFKRAFQRLCCARRAAC	386	
QY	341	PREQASLASLSLRTSHSGRRPGLS--LQVVLPLPLP--PDSDSVDG-----	385	
Db	387	RR-----RAH--GDRPRASGCLARAGPPSPAPSDDDDDGATTPARLLEPW	434	
QY	386	--SGSSGRLRLTAQLLPG	402	
Db	435	AGCNGGTTTVDSDSSLDERG	454	
RESULT	6			
153053		beta 1 adrenergic receptor - rhesus macaque		
C:Species:	Macaca mulatta (Rhesus macaque)			
C:Date:	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_Change 13-Aug-1999			
C:Accession:	I53053			
R:Searles,	R.P.; Nipper, V.J.; Machida, C.A.			
DNA Seq.	4, 231-241, 1994			
A:Title:	The rhesus macaque beta 1-adrenergic receptor gene: structure of the gene and			
A:Reference number:	I53053; MUID:95078456			
A:Accession:	I53053			
A:Status:	preliminary; translated from GR/EMBL/DBD			
A:Molecule type:	DNA			
A:Residues:	1-480 <RBS>			
A:Cross-references:	EMBL:X75540; NID:9510532; PIDN:CAA53226.1; PID:9510533			
C:Superfamily:	vertebrate rhodopsin			
C:Keywords:	neurotransmitter receptor			
Query Match	24.6%	Score 563.5	DB 2	Length 480
Best Local Similarity	34.5%	Pred. No. 3,2e-36		
Matches 149	Conservative 62	Mismatches 166	Indels 55	Gaps 14
QY	1	MVPEGPPTANSTPAMGAGPPSAPGSGWVAA--ALCVIALTAANSLLALICTOPAL	57	
Db	33	LVP--ASPPASLTPASEP--EPLSQOWTAGMGLLIALIVLVVGVVIVAIKTPRL	89	
QY	58	RNTSNFVLVSLETSDLWGVVMPMPALNLYGKRVYALRGCLLTWTFADVWCCSASITNL	117	
Db	90	QTLTNLFIMSLASADLMVGLLVPEGATIVWGRWEXGFEFLMTSDVLCVVASIETL	149	
QY	118	CLISLDRLLLTSLPRYKRYLNTPLRALALVGAWSLAALASFLLTLGW--HELGHKRPV	175	
Db	150	CVIALDRLATSPFRQOSLITRARAALVCTVMAISALVSFLPLMHMMRAESEDARRC	209	

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OY      176 V--PCGCRLLASLPFLVVASGLTFELPSGAICFTFYCRILLAAKQAVOVAS----LTGM    229
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      210 YNDPNCOCDEVTRRAALAIASVSFYPPLICMAFVLVLRERQKYKKIDCSERRFLGP    269
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      230 ASQASET-----LOVPRTPRGVESADS-----RLATKHSRALKAK    267
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      270 AAPSPSPSPSPSPVPAPPPRPAAMAAATAATPLVNGCRACKRRSPRALRECKALK--    327
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      268 LTLGLILGFEMFTWLPPEFVANIVQAV-CDGISPGLEVDLVTWLYGYCNSTMPNPIITY---PLF    323
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      328 -TLGIIMGVFTLCMLPEFLANVVKAFHRELVDRLVFEPFNIGVANSAPNPILTYKRSP--    384
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      324 MDEFRALGRFLPCRPCRPERRQASLASPSLRTSHSGPREGLSLQQVLPPLP-PDSSDS    382
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      385 --DFRNAFORLLCCARRAARRHAHGDRPRASGCILARPG-----PPSRGAASDDDD    435
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      383 DAGSGSSGLRL    394
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      436 DDVGATOPARL    447

RESULT 7
ORRHU1
beta-1-adrenergic receptor - human
C.Species: Homo sapiens (man)
C.Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 22-Jun-1999
C.Accession: A39911
R.Fiettelie, T.; Collins, S.; Daniel, K.W.; Caron, M.G.; Lefkowitz, R.J.; Koblika, B.K.
Proc. Natl. Acad. Sci. U.S.A. 84, 7920-7924, 1987
A.Title: Cloning of the cDNA for the human beta-1-adrenergic receptor.
A.Reference number: A39911; MUID:88068509
A.Accession: A39911
A.Molecule type: mRNA
A.Residues: 1-477 <FRI>
A.Cross-references: GB:J03019; NID:g178199; PIDN:AAA5167.1; PID:g178200
C.Genetics:
A.Gene: GDB:ADRB1; ADRB1R
A.Cross-references: GDB:119654; OMIM:109650
A.Map position: 10q25-10q25
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:58-84/Domain: transmembrane #status predicted <TM1>
F:94-121/Domain: transmembrane #status predicted <TM2>
F:133-154/Domain: transmembrane #status predicted <TM3>
F:177-199/Domain: transmembrane #status predicted <TM4>
F:224-245/Domain: transmembrane #status predicted <TM5>
F:325-346/Domain: transmembrane #status predicted <TM6>
F:358-377/Domain: transmembrane #status predicted <TM7>
F:358-377/Domain: transmembrane #status predicted <TM7>
F:358-377/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          24.3%   Score 557; DB 1; Length 477;
Best Local Similarity 33.8%; Pred. No. 1e-35;
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;

OY      1 MYPEEGPTANSTRPWAGCAPSPAPGSGWVAALCVIALTAANSLLIALICTOPALRNTP    60
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      33 LVPAASPASLIAPPASESEPISLQQTAGKGLMALIYLIVLVANGNLVALAIATKPRIQLT    92
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      61 SNFFLSVLFSTSLMAGLVVMPAMPNALYGKRYLARGLCLMTAFDVMCCSASIIINLCII    120
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      93 TNLFITMSIASADLVGLLVLPFGATIVWGMRXESFCCEIMTSVDVLCVTAASIEITLCVI    152
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      121 SLDRYLLTILSPIRYLYRMYLPRLALALVYGANSLLIAFLPLLGLW--HEIGHARPV--    176
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      153 ALDRILAITSPRRYSOLITRARARGLVCTVWATISLVSFLLTHMMWRRESDEARCYND    212
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      177 PGQCRLLASLPFLVVASGLTFELPSGAICFTFYCRILLAAKQAVOVAS----LTGMASQ    232
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      213 PRCDCPFVNRAVAIASVSFYPPLICMAFVLVLRERQKYKKIDCSERRFLGGPARP    272
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      233 ASET-----LOVVRTPRGVESADS-----RLATKHRSKALKAKLTITCIL    273
|       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      273 PESPSPVPAPAPPPGPPPPAATAATAPLANGRACKRRRPSRLVALREKALK---TLGI 329
QY      274 LGMFEVTVLPFFVANIVQA-CDICISPGFDVLTWLGICNSIMNPITY----PLENRDFKR 329
       : : : | | | | | : | : | : | | | | | | | | | | | | | | | | | | |
Db      330 MGVFTLCWLPFLAVVAFAFHRELVPDRLEFVFNNLGYANSAFNIIYCRRP---DPRK 385
QY      330 ALGRFLPCRCRERQASIASPLRTSHSGPPPGSLTQQVLPPLP-PDSODSDAGSGG 388
       | : | : | : | : | : | | | | | | | | | | | | | | | | | | |
Db      386 AFQGILCCARRARRRRHATHGDPRASGCLARFG-----PPSPGAASDDDDDDVVGA 438
QY      389 SSGRLR 394
       : : | |
Db      439 TTPARL 444

RESULT      8
S65459
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999
C:Accession: S65459; S40504; S31659
R:Pictiri-Rouxel, F.; Lenzen, G.; Kepoor, A.; Drumare, M.F.; Archimbault, P.; Strosberg
Eur. J. Biochem. 230, 350-358, 1995
A>Title: Molecular cloning and pharmacological characterization of the bovine beta3-a
A:Reference number: S65459; MUID:95324546
A:Accession: S65459
A:Molecule type: mRNA
A:Residues: 1-405 <PIE>
A:Cross-references: EMBL:X85961; NID:9757758; PIDN:CMA59937.1; PID:9757759
A:Experimental source: brown adipose tissue
R:Castella, L.; Muzain, P.; Revelli, J.P.; Riquier, D.; Giacobino, J.P.
Biochem. J. 297, 93-97, 1994
A>Title: Expression of beta(1)- and beta(3)-adrenergic-receptor messages and adenylylat
ite fat.
A:Reference number: S40503; MUID:94107292
A:Accession: S40504
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 162-298 <CAS>
R:Stiofel, B.; Meyer, H.H.D.
submitted to the EMBL Data Library, June 1992
A:Description: Bovine beta3-adrenergic receptor, partial genomic sequence.
A:Reference number: S31659
A:Accession: S31659
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 4-5, 'HE', 8-105 <STO>
A:Cross-references: EMBL:X67214
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; trans
F:327-343/Domain: transmembrane #status predicted <TM1>
F:773-101/Domain: transmembrane #status predicted <TM2>
F:713-113/Domain: transmembrane #status predicted <TM3>
F:1156-119/Domain: transmembrane #status predicted <TM4>
F:204-225/Domain: transmembrane #status predicted <TM5>
F:293-314/Domain: transmembrane #status predicted <TM6>
F:327-347/Domain: transmembrane #status predicted <TM7>
F:8,26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      24.2%, Score 554; DB 2; Length 405;
Best Local Similarity 33.6%; Pred. No. 1,56-35;
Matches 143; Conservative 61; Mismatches 156; Indels 66; Gaps 13; .

QY      1 MYPEEG-PTANSTRAMWGCPSPAGSGVAAALCVIATLPAANSLLIALTCQPALRN 59
       : : : | | | | | : | : | : | : | : | | | | | | | | | |
Db      11 LTPWDIPTLATPNPTANASGLPGVPWAVALACALLATALATLVATGNGNLITVAIARTPRLOT 70
QY      60 TSNFELVLFSPDSLVGVLVMPPALNLVGRWLVARGLCLMLTAFPDWCCSASTLNCL 119
       : : : | | | | | : | | | | | | | | | | | | | | | | | |
Db      71 MTNVETVSLATADLVGLLVYPGGATLTALTGHMPLGVTGCELMTSVDIVCYTASTIEFLCA 130
QY      120 ISLRVYLILLSIPRYKRLMRPLRALAIVLGAMSIAALASFLDLLLGWHELG-----H 171

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Db      131  LAYDRYLAVINPLRYGALVYTKRRALLAAVYLWVWVVAASAFAPIMSKWMWMLIGDAERQKCH 190
QY      172  ARPPVPGQCRLLASLPVULVAGSLTFPPDLSGALCTFYTCRIILAAKQAVOVALTTGM-- 229
Db      191  SNPRC---CTFASNMPPALLSSVSSEYLLPLVLVLFYVAVFVAVATQ--LRLRLRELGRFP 246
QY      230  -----ASQASRTLDQVPTPRPGVESADSR--RLATKHSKAKAKLTIELILGMPFV 279
Db      247  PEESPPAPSSNGSGTGLGCPASAPAGVPTGRRPARRLLPREHVALK---TLGLMGTFTL 303
QY      280  TWLTFEYFANIVQAV--CDICSPGLFVULVWLYGACNSTMPDIY---PLTFMRQFKALGRF 334
Db      304  CMLPFEYVNVVNALGSGSLVSGPTFLALNNLIGYANAFNPFLITCRSPDRSFRRLDRC 363
QY      335  LP-----CPRCPRERQASLASPSLRTSHSGSPRGSLQOVLPLPLPDPDSDDSDAGS 386
Db      364  RPEEHLAASPAPRAS-----GAPLATLSPAGPMQ-----PPELD----- 398
QY      387  GGSSGL 392
Db      399  GASGGL 404

```

RESULT 9

S32804

beta-3-adrenergic receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence-revision 03-Feb-1994 #text-change 13-Aug-1999

C:Accession: S32804; S32827; S18548

R:Emorine, L.J.

submitted to the EMBL Data Library, March 1993

A:Reference number: S32803

A:Accession: S32804

A:Molecule type: DNA

A:Residues: 1-400 <EMO>

A:Cross-references: EMBL:X72862; NID:g298112; PIDN:CAA51384.1; PID:g298113

R:van Sprosen, A.; Nahmias, C.; Rieff, S.; Briand-Sutren, M.M.; Strosberg, A.D.; Emorine, L.J. Biochem. 213, 1117-1124, 1993

A:Title: The promoter and intron/exon structure of the human and mouse beta3-adrenergic

A:Reference number: S32826; MUID:93279311

A:Accession: S32827

A:Molecule type: DNA

A:Residues: 1-8:341-347; 380-400 <SPR>

R:Nahmias, C.; Blin, N.; Elalouf, J.M.; Mattei, M.G.; Strosberg, A.D.; Emorine, L.J. EMBO J. 10, 3721-3727, 1991

A:Title: Molecular characterization of the mouse beta-3-adrenergic receptor: relationship

A:Reference number: S18548; MUID:92037534

A:Accession: S18548

A:Molecule type: DNA

A:Residues: 1-388 <NAH>

A:Cross-references: EMBL:X60438; NID:g50109; PIDN:CAA42966.1; PID:g50110

C:Genetics:

A:Map position: 8A2-4

C:Introns: 388/2

C:Superfamily: G protein-coupled receptor; glycoprotein; transmembrane protein

C:Keywords: G protein-coupled receptor; status predicted <TM1>

E:37-60/Domain: transmembrane #status predicted <TM1>

F:70-98/Domain: transmembrane #status predicted <TM2>

F:110-130/Domain: transmembrane #status predicted <TM3>

F:153-170/Domain: transmembrane #status predicted <TM4>

F:201-222/Domain: transmembrane #status predicted <TM5>

E:290-311/Domain: transmembrane #status predicted <TM6>

F:324-344/Domain: transmembrane #status predicted <TM7>

E:326/Blinding site: carbohydrate (Asn) (covalent) #status predicted

```

Db      3  PMPHRNGSLAAMSDAPPLIDPESAANTSGLPGVPMMAALAGALLALATVGGNMLVIALART 62
Oy      55 PALRNTSNFELVLSFTSDLMVGLVMPMPAMINALYGRKVLARGLCLLMTAFI WHCCSAST 114
Db      63  PRIQITIVFVSTLAADLVILGMLMPGATLALTGMHPGIGETCEIAMTSVIVLCVASTI 122
Oy     115  LNLCLISIDRVLILSLPRKYLRMTPTLRALALVIGAMSLAASLEPLILGWHELG---- 170
Db     123  ETLCLALVDRILVATNPRLRGITVYTKRARAAYLVIVISAASFAPIMSQMMRWGADAE 182
Oy     171  ----HARPVPGOCRLTSLAEFLVVASGLFPEPLSGAICETFYCRILLAAKROAVASLT 226
Db     183  AOECHSNRC---CSFASNMRYALLSSVSSTYEDPLMLVLYARFVYARQR--HLIRE 238
Oy     227  TGMASQASLETQVBRTPRP-----GVESADR--RLATKHSKALKARLTLTGILL 274
Db     239  LGRFSESPSPSPSPSPATGATGPAPADGVPCCGRPRARLLPLREHRAIR---TLGLIM 295
Oy     275  GMFEFTWLPFEVVANIVQAVC--DCISGLPEVULVWLGCGNSTAMPILY----PLEMRBFKR 329
Db     296  GIFSLCWLPEFLVAVLRLALAGPSLVPSGCVFLTAMWLDGYANSAFNPIYICRSPDFROAFRR 355
Oy     330  AL-----GRFLCPRC---PREQOASLASPSLR--TSHSGRRP 362
Db     356  LLCSTYGGGPEEPRAVYTFPASPVAAROSPPLNRDGTDEGARP 397

```

RESULT 10  
DYNH1D1  
dopamine receptor D1 - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 22-Jun-1999  
C:Accession: S11377; S11376; S11379  
R:Zhou, Q.Y.; Grandy, D.K.; Thambi, L.; Kushner, J.A.; van Tol, H.H.M.; Cone, R.; Pri  
Nature 347, 76-80, 1990  
A>Title: Cloning and expression of human and rat D(1) dopamine receptors.  
A:Reference number: S11377; MUID:90370094  
A:Accession: S11377  
A:Molecule type: DNA  
A:Residues: 1-446 <ZHO>  
A:Cross-references: EMBL:X58987  
R:Derry, A.; Gingrich, J.A.; Paladeu, P.; Freneau Jr., F.L.; Bates, M.D.; Caron, M  
Nature 347, 72-76, 1990  
A>Title: Molecular cloning and expression of the gene for a human D(1) dopamine recep  
A:Reference number: S11376; MUID:90370093  
A:Accession: S11376  
A:Molecule type: DNA; mRNA  
A:Residues: 1-446 <DEX>  
A:Cross-references: EMBL:X55760; NID:g30396; PIDN:CAA39286.1; PID:g30397  
R:Sunahara, R.K.; Niznik, H.B.; Weiner, D.M.; Stormann, T.M.; Brann, M.R.; Kennedy, J  
Nature 347, 80-83, 1990  
A>Title: Human dopamine D(1) receptor encoded by an intronless gene on chromosome 5.  
A:Reference number: S11379; MUID:90370095  
A:Accession: S11379  
A:Molecule type: DNA  
A:Residues: 1-446 <SUN>  
A:Cross-references: GB:X55758; NID:g288931; PIDN:CAA39284.1; PID:g288932  
C:Genetics:  
A:Gene: GDB:DRD1  
A:Cross-references: GDB:125240; OMTM:126449  
A:Map position: 5q34-5q35  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter r  
F:1-87/Domain: transmembrane #status predicted <TM1>  
F:98-119/Domain: transmembrane #status predicted <TM3>  
F:140-163/Domain: transmembrane #status predicted <TM4>  
F:194-214/Domain: transmembrane #status predicted <TM5>  
F:215-273/Domain: intracellular #status predicted <CY7>  
F:274-295/Domain: transmembrane #status predicted <TM6>  
F:313-333/Domain: transmembrane #status predicted <TM7>  
F:5-175/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:96-186/Disulfide bonds: #status predicted

F;136,268/Binding site: phosphate (Thr) (covalent) #status predicted  
F;259,263/Binding site: phosphate (Ser) (covalent) #status predicted  
F;347/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match	24.1%;	Score 552.5;	DB 1;	Length 446;
Best Local Similarity	31.2%;	Pred. No. 2.1e-35;		
Matches 143;	Conservative 79;	Mismatches 172;	Indels 65;	Gaps 13;

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0Y 21 SAPPSSGVW-----AAALCVYALTPAANSNLTALICITOPALRN-TSNFFVSL 68
Db 7 SAMDQGTGLVERDFSVRIITLQACFLISLILSLTGLNLTIVCAAVINFRHLRSKVTNFVYISL 66
0Y 69 PFSDLMAVOLVMPRPMALNALLYGRWYLAGCLLMTADVWCCSAILNCLISIDRLTL 128
Db 67 AVSDDLVLVALVMPKMAVAEIGAFWPFQ-SFQNIWVADIDIMQSTASILNLCVTSYDRWMAI 1255
0Y 129 LSPLEKYLRMPRLRLALAVLAMSIAALASLUPLLGLMHELGHARPPVPG----- 178
Db 126 SSPFEYERKMTPKAFLILISAMTILSVLSTIPQLSNHK---AKPLSPSDGNATSLAET 162
0Y 179 --QCRLLASLPEFVLVNASGLTFEELPSGACITFYCRILLLAARQAAOVASL--TTGMSQASE 2355
Db 183 IDNCSSLSRTYAISSVYSIFYPALIMIVYTRYLRQAQOIRIALEBRAVAHANQC 2422
0Y 236 TLQVYRTRPGVESADSRRLTKHSRAKAKLLGLILGMEFYTWLPRFYANIVQAVCD 2395
Db 243 TTTGNGKREVECSQPSSEFSKMFKRETKYLK--TLVSIMGVYFCWMLPFLLNCLPFCG 299
0Y 296 -----CISQGLPFVLLWLYGCVNSTMPRIITYPLFMDRFRKALGRPLPCPR-CPREQA- 346
Db 300 SCEIOPFCIDSTFPEYFVFWEGHANSLSMPITY-AFMADFRKAEFTLLGCTYRLCPATNNAI 358
0Y 347 -----SLASPLRTSHSGPRGELSLOQVYLPRLPPDSDDSDAGSGSSGLRLTAQQLP 401
Db 359 ETVSINNNGAMFSSHHHPRGISISECNLYVILPHAVGSSEDLKEKBAAGIARLEKLS 418
0Y 402 GEAOTDPLPLPRAAAVAVFNIDPAEBELRP-----HP 434
Db 419 -----ALSVLIDYDTIVLSLEKTOPIQNGQHP 445

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RESULT 11  
AA1679  
beta-3-adrenergic receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 13-Aug-1999  
Accession: AA1679  
Muzallin, P.; Revelli, J.P.; Kuhne, F.; Gocayne, J.D.; McCombie, W.R.; Venter, J.C.; Gitlin, D.; Schaeuble, C.; White, O.; Adams, M.D.; Venter, A.; Bol. Chem. 266, 24053-24058, 1991  
A:Title: An adipose tissue-specific beta-adrenergic receptor. Molecular cloning and down  
A:Reference number: AA1679; MUID:92084710  
A:Accession: AA1679  
A:Molecule type: mRNA  
A:Residues: 1-400 <MUD>  
A:Cross-references: GB:M74716; NID:9950087; PIDN:AAA74470.1; PID:9202766  
A:Experimental source: brown adipose tissue  
A:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	24.1%	Score 551.5:	DB 2:	length 400:
	Best Local Similarity	35.8%:	Pred. No. 2.3e-35:		
	Matches 144:	Conservative 61:	Misnomers 146:	Indels 51:	Gaps 15:
Oy	5	PGPANTSFA-GGAGP----	PSARGSG-----	VWAALCVIAL--TAANSLLILICIQ	54
Db	3	PAPHRNGSLAEFSDAPTLDPSAANTSGLEGPWAAALACALIALATLVGGNLLVYTAIAIT			62
Oy	55	PALRMTSNFEFLSFTSDLMGLVAMPMLNALGRWLARGCLLTAFDPMCCSAI			114
	:   :				
Db	63	PLQGITTNVEFVSLTADLVGLVLPPEPATLAIQHMPLGATGCGLMTVDVLCTYASI			122

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OY      115  INLCISIDRLLLSIPRYLIRMTPERALALYVGAASLAASFLPLGLGMIHLG---- 170
Db      123  ETLCLAVDRYLAVYNPLRGVLTITKRRARAAYLVIMIVSATVSPAFIMSGMMHVGADAE 182
OY      171  ----HARPPVGOCRLLASLPFVLVASGLFFLPSCAICTTCHILLAARKAOV---- 222
Db      183  AOECISNRC--CSFASNMRYALILSSSVSYFLPLVMEVYARFVFAVRAKRRFVAREL 239
OY      223  -----ASLTGGMASOASETLOVPRTPRGVESADSR--RLATFHSKALKAKLTGIL 274
Db      240  GRPEEESPRSPSPSPATVGP-TASDVGPSGCRRAPLPLGEHRAIR---TGLIM 295
OY      275  GMEFYTWLPFVAVNIQVAVC--DCISGLEDVLTWLCYCNSTANPIY---PLFMRDFKR 329
Db      296  GIFSLCWTLPFLAVLWRLVWPSLYVPGVFALIMWLGYANSAFNPILYCRSPDFRAFR 355
OY      330  AL----GREFLCPRC---PREROASLASPSLR--TSHSGRP 362
Db      356  LLCSTGGGPEEPKRVYTFPASPASRONSPLNRDGTGEGERP 397

```

RESULT 12  
A53281  
beta 3-adrenergic receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-May-1994 #sequence, revision 18-Nov-1994 #text, change 13-Aug-1999  
C:Accession: A53281; S29808  
R:Granneman, J.G.; Lahners, K.N.; Chaudhry, A.  
Mol. Pharmacol. 40, 895-899, 1991  
A:Title: Molecular cloning and expression of the rat beta 3-adrenergic receptor  
A:Reference number: A53281; MUID:92100057  
A:Accession: A53281  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-400 <GRA>  
A:Cross-references: GB:S73473; NID:g2a1215; PIDN:AAB20702.1; PID:g2a1216  
A:Note: Sequence extracted from NCBI backbone (NCBIN:73473, NCBI:P73476)  
R:Bensaid, M.; Kaghad, M.; Rodriguez, M.; le Fur, G.; Caput, D.  
FEBS Lett. 318, 223-226, 1993  
A:Title: The rat beta3-adrenergic receptor gene contains an intron.  
A:Reference number: S29808; MUID:93178631  
A:Accession: S29808  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-400 <BEN>  
A:Cross-references: GB:S56481; NID:g298306; PIDN:AAB25520.1; PID:g298307  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	24.1%	Score 551.5	DB 2:	Length 400:
Best Local Similarity	35.3%	Pred. No. 2.3e-35:		
Matches 142:	Conservative	61:	Mismatches 148:	Indels 51:
				Gaps 15:
QY	5	PGPTANSTPA-WGAGP-PSAAGSG-----WVAALCVIAL-TAAANLILICTQ	54	
DB	3	PMPHKNSLAFMSDAPITDDPSAANTSGLPVPMALAGALLATATVGCNLLVITAIART	62	
QY	55	PALRNTSNEFLVLEFSTDMLVGLVYMPRLMALNYGRWYLGCLLTAFDYMCSSASI	114	
DB	63	PLRQITITVFYSLATADLVGLVLMPPRATLALGHMPLGATGELMTSVGLCVTASI	122	
QY	115	INLCISIDRYLLIISPRYKLRMTPLRLALAVLGMSLAALASFLPLIGMHELG----	170	
DB	123	ETLCLAVDRYLAIVNPLRTGLVTKRRRAAVLVLMYISATVSTAPISOMHRRGADAE	182	
QY	171	---HARPPVGQCRLLASLPFLVYASGLTFELPSGAICFTYCRILLARKQAVOYASLT	226	
DB	183	AQCHSNDRPC---GSFASNMYPALLSSSVSYFLPLVLMFLVAVRFPVAKQR-RLRRE	238	
QY	227	TGMAQASSETLVQPTPRP-----GVSSADR-RLATKSRKRLAKKLTLGILL	274	



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C:Genetics:
A:Introns: 402/1
C:Superfamily: vertebrate rhodopsin

Query Match      23.7%; Score 543.5; DB 2; Length 418;
Best Local Similarity 34.0%; Pred. No. 9,8e-35;
Matches 144; Conservative 63; Indels 63; Gaps 15;

Oy      1 MYPEEG-FPIANSTPMAGGAPSPAPGSGGVAALCVILTAANSLLALICTOPALRN 59
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      11 LVPMPDVLPLAAPTANTSGLPVMAAALAGALLALAVLATVGGNLIVALTPTPTLOT 70
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      60 TSNFPLTSLFTSDLLWGLVMPMPAMLMNXGMVTLARGCLIMFPAFDVCCSASTINLCL 119
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      71 MIVNVTSLAAMDVLWGLLVPPAATLVLTGMPDAGATCCELMSTSDVLCVTASETTCA 130
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      120 ISLDREYLLISPLRYKRLKMTPLRALATLVGAASLALASFLDLLGHELG-----H 171
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      131 LAVDRYLAVTNPLRGALVTKRRARAAYLVWVYSAASVAFPIMSQMKRWGDAEAGRGH 190
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      172 ARPPVPGCCRLIASLPVLVAGSLFFELPSGAICFTYCRILLARQAVVASLTGGM-- 229
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      191 SNPRC---CAFASNMPPVYLLSSVSPYPLTLVLMFYAVFVAVTRQ--LRLRMELGRPP 246
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      230 ASQASETTLQVPTPRP-----GVESASDR--RLATHSKKALKAKLTGLTGLGMFEV 279
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      247 PEESPSPALSRSLAPAPAGTCAPEGVPAACCRPARLLPLREHKALE---CTLGLIMGTFTL 303

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Q7 208 INTERLEUKIN-6 CSFOL  
Db 304 CMLPEFLANVLRALG---GPSLVPDPAPFLAFLNMGAYANSAPNPLLYCKSPDFRSAFRRL 360  
QY 332 ---GFFLCPCPRCPREQAASLPSSLTSTSHSGRPGLSLQQVLPFLPDPSSDSDAGSGG 388  
Db 361 CHCGGRLLRREFCAPADRPASSFRAPL-----RRG-----PAPRSFGFAS-----G 399

QY 389 SSSL 392  
||:  
||:  
Db 400 STGL 403

RESULT 15  
147217  
dopamine receptor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 13-Aug-1999  
C:Accession: I47217  
R:Grenader, A.C.; O'Rourke, D.A.; Healy, D.P.  
Mm. J. Physiol. 268, F423-F434, 1995  
A:Title: Cloning of the porcine D1A dopamine receptor gene expressed in renal epithel  
A:Reference number: I47217; MUID:95208810  
A:Accession: I47217  
A:Status: preliminary; translated from GB/EMBL/DDBU  
A:Molecule type: DNA  
A:Residues: 1-446 <GRE>  
A:Cross-references: EMBL:U25681; NID:g808097; PIDN:AAA79848.1; PID:g808098

[illegible]



Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	2025	88.4	438	11	063004	063004	rattus norvegicus
2	578	25.2	405	11	Q9CRR2	Q9CRR2	mus musculus
3	563.5	24.6	405	6	Q9GJ56	Q9GJ56	ovis aries
4	559.5	24.4	405	6	Q9GJ56	Q9GJ56	ovis aries
5	558.5	24.4	405	6	Q9GJ70	Q9GJ70	ovis aries
6	556	24.3	405	6	Q9GJ57	Q9GJ57	ovis aries
7	546.5	23.8	402	5	044198	044198	apis mellifera
8	540.5	23.6	407	6	Q9M200	Q9M200	sus scrofa
9	535	23.3	445	13	Q98841	Q98841	anguilla anguilla
10	528	23.0	446	13	042315	042315	cyprinus carpio
11	525	22.9	385	5	Q24038	Q24038	drosophila melanogaster
12	524	22.9	427	13	042316	042316	cyprinus carpio
13	523.5	22.8	331	5	Q96716	Q96716	branchiostoma lanceolatum
14	511.5	22.3	445	13	Q98842	Q98842	anguilla anguilla
15	509.5	22.2	559	11	Q9QW71	Q9QW71	rattus norvegicus
16	503	21.9	339	5	Q9NG02	Q9NG02	apis mellifera
17	501	21.9	511	6	Q9TMM9	Q9TMM9	sus scrofa
18	496	21.6	418	13	Q98844	Q98844	anguilla anguilla
19	493.5	21.5	477	5	Q9BMA9	Q9BMA9	mamestra brassicae

20	491.5	11.4	380	13	042317	042317	cyprinus	glut
21	491	21.4	392	13	09VHA5	09VHA5	myxine	glut
22	488.5	21.3	394	5	09NHR3	09NHR3	aplysia	cal
23	488	21.3	419	5	077254	077254	boopis	am
24	487.5	21.3	458	13	098843	098843	anguilla	an
25	485	21.2	518	13	042318	042318	cyprinus	ca
26	483.5	21.1	584	6	09MY18	09MY18	oryctolagus	ca
27	483	21.1	515	17	09DBL0	09DBL0	mus	musculu
28	481.5	21.0	508	5	09VC33	09VC33	drosophila	
29	472.5	20.6	470	11	P97842	P97842	rattus	norv
30	471.5	20.6	394	4	09NJS6	09NJS6	aplysia	kur
31	468	20.4	466	11	09WU25	09WU25	cavia	porce
32	464.5	20.3	464	5	09GQ54	09GQ54	aedes	aegyp
33	463	20.2	466	6	09TSM7	09TSM7	sus	scrofa
34	462	20.2	359	9	09H139	09H139	homo	sapien
35	460.5	20.1	397	11	09D282	09D282	mus	musculu
36	458.5	20.0	358	11	09OX37	09OX37	mus	musculu
37	458	20.0	429	4	013729	013729	homo	sapien
38	458	20.0	499	4	013675	013675	homo	sapien
39	457	19.9	468	4	09UD53	09UD53	homo	sapien
40	454.5	19.8	406	13	098598	098598	xenopus	lae
41	453	19.8	471	11	09OM77	09OM77	cricketula	
42	450.5	19.7	377	6	09NM53	09NM53	sus	scrofa
43	450.5	19.7	425	6	09MZU2	09MZU2	oryctolagus	
44	450.5	19.7	429	6	09MZU3	09MZU3	oryctolagus	
45	450	19.6	455	4	060451	060451	homo	sapien

## ALIGNMENTS

RESULT	1	
063004		
ID	063004	PRELIMINARY;
AC	063004	PRT; 438 AA.
DT	01-NOV-1996	(TREMBLrel. 01, Created)
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)
DE	5-HT6 SEROTONIN RECEPTOR.	
OS	Rattus norvegicus (Rat).	
CC	Euryarchaeota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN STRIATUM;	
RX	MEDLINE=96102917; Pubmed=8522988;	
RA	Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E	
RA	Meltzer H.Y., Sibley D.R., Roth B.L., Hamblin M.W.,	
RT	"Cloning, characterization, and chromosomal localization of a human	
RT	5-HT6 serotonin receptor.";	
RL	J. Neurochem. 66:47-56(1996).	
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL; L41146; AAA92633.1; -	
DR	InterPro; IPR000276; GPCR_Rhodopsn.	
DR	Pfam; PF00001; 7tm_1; 1.	
DR	PRINTS; PR00237; GPCRHHODOPSN.	
DR	PROSITE; PS00237; G_PROTEIN_RECP_FL1; 1.	
DR	PROSITE; PS02623; G_PROTEIN_RECP_FL2; 1.	
KW	G-protein coupled receptor; Glycoprotein; Transmembrane.	
SO	SEQUENCE 438 AA; 46786 MW; DB90403892F091A9 CRC64;	

Query Match	88.4%	Score 2025;	DB 11;	Length 438;
Best Local Similarity	88.9%	Pred. No. 4.3e-136;		
Matches 391;	Conservative 12;	Mismatches 35;	Indels 2;	Gaps 1

QY	Db	QY
1	1	61
MYPEEGPAPNASTPAMGAGPPAPGSGGVMVAALCVCVTLTAAPNANSLIALICQPAALNT	MYPEEGPAPNASTPAMGAGPPAPGSGGVMVAALCVCVTLTAAPNANSLIALICQPAALNT	SNFELVLSFTSDLWGLVMPAPMALMALYGRWLTARGCLLTIAFDVMCCSASILNLCLI
60	60	120

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Db 61 SNFFVLSFLSDLMGLVMPVPMNLNKLGRWMLARGLCLMTAFDWCSSASTLNCIL 120
QY 121 SLDYVLLISPLRYKLRMPPLRALALVLAGMSLAALASFLPLLLGHELGHARPVYGQC 180
Db 121 SLDYVLLISPLRYKLRMPPLRALALVLAGMSLAALASFLPLLLGHELGHARPVYGQC 180
QY 181 RLASLPFVYVAGLTFPLPSGALCFYCYCILLARQAVASLTGMAASQSEPLQVP 240
Db 181 RLASLPFVYVAGLTFPLPSGALCFYCYCILLARQAVASLTGMAASQSEPLQVP 240
QY 241 RPRPVEASDRRLATKHSRKLAKLTLTGILGFEVWLPPEPVANITQAVQDCISPG 300
Db 241 RPRPVEASDRRLATKHSRKLAKLTLTGILGFEVWLPPEPVANITQAVQDCISPG 300
QY 301 LFDVLTWLGVCNSTMPRIYPLFMRDFKRALGFRPCPRCPRROASLASPLRTSHSGP 360
Db 301 LFDVLTWLGVCNSTMPRIYPLFMRDFKRALGFRPCPRCPRROASLASPLRTSHSGP 360
QY 361 RPLGLSLQOVLPLPLPDSDSDSAGSGSGLTLTAQLLPGATODPPLPTAAAVNF 420
Db 361 RPLGLSLQOVLPLPLPDSDSDSAGSGSGLTLTAQLLPGATODPPLPTAAAVNF 420
QY 421 FNIDPAEPPLRPHLGIPTN 440
Db 421 FNIDPAEPPLRPHLGIPTN 440
QY 419 FVTVDSVEPELRPHRPLSSPVN 438
Db 419 FVTVDSVEPELRPHRPLSSPVN 438

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RESULT 2
Q9CRR2 PRELIMINARY; PRT: 405 AA.
AC 09CRR2:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE ADRENERGIC RECEPTOR, BETA 1 (FRAGMENT).
GN ADRL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada S.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AK018378; BAB31185.1; -
DR MGD: MGI:87937; Adrb1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_3; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_4; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_5; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_6; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_7; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_8; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_9; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_10; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_11; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_12; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_13; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_14; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_15; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_16; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_17; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_18; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_19; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_20; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_21; 1.
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DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT NON_TER
SQ SEQUENCE 405 AA; 44741 MW; 4F0F3PBB956E2F4 CRC64;

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Query Match 25.28; Score 578; DB 11; Length 405;
Best Local Similarity 36.58; Pred. No. 1.6e-33;
Matches 150; Conservative 61; Mismatches 140; Indels 60; Gaps 15;

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QY 33 LCVVIALTAANSLIALICTOPALRNTSNFVLSFTSDLMGLVMPVPMNLNKLGRW 92
Db 4 LALIVLTIVGNLVVIAIAKTRPLRLTLNLTNLSADLVGLVPEGATVWGRW 63
QY 93 VLARGCLMTAFDVMCCSASIIINLCISDRYLILISPLRYKLRMPPLRALALVLAGMS 152
Db 64 EYSGFCELTSTVDLCVNTASIEFLCVIALDRILATSPRRYOSLTLRAARALVCTVNA 123
QY 153 LALASFLPLILGW--HELGHARPV--PGCRLASLPFVYVAGLTFPLPSGALCFY 208
Db 124 ISALVSFLPLIMHMMRAESDEARCYNDPKCDFVTRAYAIASVVSFVPLCIMA 183
QY 209 CRILAAKQAVOVS---LTTGMAASQAS-ETLQVPRPVEASDR-----RLA 256
Db 184 LRVRERAKQVKKIDSCERFLGPARPPSPSPGPRPADSLANGRSSRRRPSRLV 243
QY 257 TKHSRRALAKTLTGILGFEVWLPPEPVANITQAV-CDICISPLGFDVLTWLGVCNSTM 315
Db 244 ALREOKALK---TLGILGFEVWLPPEPVANITQAV-CDICISPLGFDVLTWLGVCNSTM 300
QY 316 NPITY---PLFMDRFRALGFRPCPRCPRCPRROASLASPLRTSHSGPRLGSL--LQ 367
Db 301 NPITYRSP---DFRKARQLCCARRACRR-----RAAH-GDRPRASGCLA 344
QY 368 QVPLPLP--PDSDSDSAG-----SGSSGSLRTAQLLPG 402
Db 345 RAGPPSPGAPSDDDDDAGTTTPARLLEPMTCNGGTTIVDSDSLDEPG 395

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RESULT 3
Q9GL56 PRELIMINARY; PRT: 405 AA.
AC 09GL56:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BETA 3 ADRENERGIC RECEPTOR.
GN B3AR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN 11
RP SEQUENCE FROM N.A.
RC Porrest R.H., Hickford J.G.H.;
RT "Polymorphism within the ovine beta 3 adrenergic receptor gene.";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF314203; AAG31166.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
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Query Match 24.88; Score 563.5; DB 6; Length 405;
Best Local Similarity 34.88; Pred. No. 1.7e-32;
Matches 146; Conservative 56; Mismatches 163; Indels 55; Gaps 13;

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[illegible]

RESULT	4
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ID	09GJS6 PRELIMINARY; PRT; 405 AA.
AC	09GJS6;
DT	01-MAR-2001 (TREMBLrel, 16, Created)
DT	01-MAR-2001 (TREMBLrel, 16, Last sequence update)
DT	01-JUN-2001 (TREMBLrel, 17, Last annotation update)
DE	BETA 3 ADRENERGIC RECEPTOR.
GN	B3AR.
OS	Ovis aries (Sheep).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Caprinae; Ovis.
OX	NCBI_TaxID=9940;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Forrest R.H., Hickford J.G.H.;
RT	"Polymorphism within the ovine beta 3 adrenergic receptor gene.";
PL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
CC	EMBL: AF114204; BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL: AF114204; AAG31167.1; -
DR	EMBL: AF314202; AAG31165.1; -
DR	InterPro: IPR00276; GPC_Rhodopsn.
DR	Pfam: PF00001; 7tm_1; 1.
DR	PRINTS: PS00237; GPCRHHDOOSN.
DR	PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR	PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SO	SEQUENCE 405 AA; 42928 MW; ADDD3ABBAF814E75 CRC64;

Query Match	24.4%	Score 559.5	DB 6	Length 405
Best Local Similarity	34.58%	Pred. No. 3.2e-32		
Matches 145; Conservative	56	Mismatches 164	Indels 55	Gaps 13

0Y 1 MYPEEG-PTANSPAMGPPSPAGSGSOWAAACVYIALTPAANSLLILICTOPLRN 59  
11 LTPMWDIETLAPNPNANSGLPGEYWAVALAGALLALAVLMTVGSNNLIYALIRPRLQT 70  
0Y 60 TSNFPLVSLFTSDLMVGLVWPPMLNALNGRWYLANGCLLMTAPFYMCSCSILNCL 119  
DB 71 MTNFEVYSLAVADIYVGLVLPAGATLALGHWPLGVGTGELMTSYDVLCVTAISIFLCA 130

[illegible]

RESULT	5	09GJUT0	PRELIMINARY:	PRT:	405 AA.
ID	09GJUT0				
AC	09GJUT0				
DT	01-MAR-2001 (Tremblrel, 16, Created)				
DT	01-MAR-2001 (Tremblrel, 16, Last sequence update)				
DT	01-JUN-2001 (Tremblrel, 17, Last annotation update)				
DE	BETA 3 ADRENERGIC RECEPTOR.				
GN	B3AR.				
OS	Ovis aries (Sheep).				
OC	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Caprinae; Ovis.				
OX	NCBI_Taxid:9940;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Forrest R.H., Hickford J.G.H.;				
RT	"Ovis aries beta 3 adrenergic receptor (B3AR) gene - allele F,				
RT	complete cds.";				
RL	Submitted (OCT-2000) to the EMBL/genbank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Forrest R.H., Hickford J.G.H.;				
RT	"Polymorphism within the ovine beta 3 adrenergic receptor gene.";				
RL	Submitted (OCT-2000) to the EMBL/genbank/DBJ databases.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL; AF314205; AAG31168.1; -;				
DR	EMBL; AF314201; AAG31164.1; -;				
DR	InterPro; IPR000276; GPCR_Rhodopsn.				
DR	Pfam; PF00001; 7tm_1; 1.				
DR	PRINTS; PR00237; GPCRHOPOPSN.				
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.				
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.				
DR	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.				
SW	SEQUENCE 405 AA; 42956 MW; 6C9FBIEBAF93C578 CRC64;				

Query Match	24.48;	Score 558.5;	DB 6;	Length 405;
Best Local Similarity	34.58;	Pred. No. 3.8e-32;		
Matches 145;	Conservative 56;	Mismatches 164;	Indels 55;	Gaps 13

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OY      1 MYPEEG -PTANSTPRMGSGPPSAGCGSQWVAALCVIATLPAANSILITICOPALRN 59
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB      11 LTPWDIFTLAPNPNNASGGLPGVPMVAVALGALLATLAVLATVGNNLEVI VAIARFPQGT 70
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
OY      60 TSNFELVSFLSDLMVGYVMPPALNALXYRWRVLARGCLTLLMVAAPMYMCSSAILMLCL 119
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB      71 MNVNVTSIATRLADLVGLLVYPGCATLTALGHMPGVGTGCELMKSVIDLCTIASILETCA 130
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
OY     120 ISLDREYLIESPURYKLRRPTLRALALVGLAMSLAALASPLPLLIGHHEUG-----H 171

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Db	131	LAVRYLAVTAVTIRGALVTRKRRARAANVLWVYSAVSEAFIMSKMMRWGADAEQRCH	190
Qy	172	ARPPPGCRLLASLPFLVVASGLTFELPSPSAICFTYCRILLARKANOV-----	2222
Db	191	SNPRC--CTFASNNPVALSSVSFTPLVLMLETVARFVAVATROLRLRLRELGRFP	247
Qy	223	-----ASLTGMSQASSETLQVPRTPPGVESADSR--RLATKHSRKALKAKITLIGLG	275
Db	248	EESPAPRSRSGSPGAG-----PYASPVGVPYSGRPARLLPLREHRLR---TLGLIMG	299
Qy	276	MEFWTWLPEFVNAVYQAN--CDGISPLGFDVLTALGCSNMNNTIY---PLFRQDKRA	330
Db	300	TFLLICWLEPFVNAVYRALGSPISVSGPTFLALNMLGYANSFNLITICRSP---DERSA	355
Qy	331	LGRELPCECRERQASLASPSLRTSHSGPPRGSLTQOVLPLPPDSDSDSPAGSGSS	390
Db	356	FRRLD-C-RCRPEEHIAASP-----PRASGATVLTLSRPGRPQSPDLGASGCLS	405
RESULT	6		
	Q9GL57	PRELIMINARY;	PRT; 405 AA.
AC	Q9GL57;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	BETA 3 ADRENERGIC RECEPTOR.		
GN	B3AR.		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;		
OC	Bovidae; Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Forrest R.H., Hickford J.G.H.;		
RT	"Polymorphism within the ovine beta 3 adrenergic receptor gene.;"		
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	EMBL; AF144200; AACG1163.1; -		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCR_RHODPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.		
DR	PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.		
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.		
NC	SEQUENCE 405 AA; 42928 MW; 6C9FE1EBAF90F54B CRC64;		

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Query Match      24.3%; Score 556; DB 6; Length 405;
Best Local Similarity 34.08; Pred. No. 5, 7e-32;
Matches 146; Conservative 59; Mismatches 151; Indels 74; Gaps

QY      1 MVEBEG-PTANSTPAMGAGPSPABGGSGWAAALCVVIALTAANAALLIALICTOPALRN 59
Db      11 LTPMEDIPPTLAPNTANASGIPGVPMVAVALGALLALAVLATVGGNLLTVIAIARTPRLQT 70
QY      60 TSNPFLVSLFSDLMGLVYVMPRLMALNLGRVWLAGLCLLRTAFVYMCSSAILMCL 119
Db      71 MTFNFFVTSLATADLVGLVGLVPPGATLALTGHWELGVTGCELMTSYVLCVTASITFLCA 130
QY      120 ISLDRIYLLISPLRKLEMPRLALALAVLIGMSSAALASFLPLLLGHWEG-----H 171
Db      131 LAVDRYLAIVNPLRYGALVYTRKRAARAIVLVYVSAVSPRIPMSKMRWRGADAENORCH 190
QY      172 ARPVPGCCRLLASLPEVYVASGLTFPELPSGALICFTYCRILLAAKQAVOY----- 222
Db      191 SNPRC---CFEASNNPVALILSSSYFYLPLLVMLFVYARFVVATRQLRLRLRELRGFRPP 247
QY      223 -----ASLTGMAASQETLVLPPTPRPGVESADSR--RLATKHSKALKAKLTLGILG 275

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Db      248  EESPAPRSGSPGAG-----PAAPGVGYSPRRPARLLPLEHRAIRL----TLGLIMG 299
QY      276  MEFVWIMPEFYANIVQAV--CDICISPLGFVDLWTWLGVCNSMNNITY--PLFMRDKRA 330
          !:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      300  TFFTCWLPFEEVNVNVRALGSPSLVSGPTFLALNMLGYANSAFNLICRSP---DFRSA 355
QY      331  LGRFPLPCRCRER-----QASLASPSLRTSHSGSPRPLSLQVYLPPLPPDSDS 382
          !::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      356  FRRLL-C-RCPPEHLAASPQAPSGAPVLTSPAPRQ-----PSRL----- 397
QY      383  DAGSGSGSL 392
Db      398  ---DGASGGL 404

RESULT 7
044198
AC      044198  PRELIMINARY; PRT; 402 AA.
AC      044198;
DT      01-JUN-1998 (TReMBLrel_06, Created)
DT      01-JUN-1998 (TReMBLrel_06, Last sequence update)
DT      01-JUN-2001 (TReMBLrel_17, Last annotation update)
DE      DOPAMINE RECEPTOR, D1.
GN      DOP1.
OS      Apis mellifera (Honeybee).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC      Apoidea; Apidae; Apis.
OX      NCBI_TaxID=7460;
RN      [1]
RN      SEQUENCE FROM N.A.
RA      Baumann A.;
RL      Submitted (MAY-1997) to the EMBL/GenBank/DDAJ databases.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL, Y13429; CAA73841.1; -
DR      InterPro; IPR00276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCR_RHODOPSN.
DR      PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; glycoprotein; Transmembrane.
SQ      SEQUENCE 402 AA; 44534 MW; 0B1962DC7E6481DF CRC64;

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	Query Match	23.88;	Score	546.5;	DB	5;	Length	402;
	Blast Local Similarity	36.44;	Prod.	No. 2.6e-31;				
	Matches	133;	Conservative	55;	Mismatches	146;	Indels	31;
					Gaps			
Qy	35	VVIALTAANSLTALICTOPALRNTSNFPLVSLETSDLWGLVMPAMLMAYGRWL	94					
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
Dd	34	ILIFLSVAGNITLCVAIYTDGRLRRIGNLFLASLAIDELFGVLIVMFAVDLGLGYWF	93					
Qy	95	ARGCLIMLTARDWCSCASILINCLISLDRIILILSPRKLRKMTPLKALALVGLANSIA	154					
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
Dd	94	GPREDDTMIADVCMSFTSASIIINCAISLDRIYIHKKDPLRGWRWTRIIAAGAIAVVLLA	153					
Qy	155	ALASLPFLMLHMHENLGARHPV-----PGOORLLASLPVYLVAAGLFPPRSGAICE	206					
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
Dd	154	GLISFVPISLHL---RANEFVULDDSKKEHPITCALDLPPIYAVSSISFPYPCIVMLG	210					
Qy	207	TTCRIILAARKQAOVAVSLT---TGNASQASETLQVPRTPRPVESADSRLATIKHSRK	262					
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
Dd	211	IYCRLYCAVQAQHVKYSIRAVTLKPDSMAKSVPVRKVHTAKPKRPQTG----KTPSYNVHS	266					
Qy	263	ALKAKLTGILLGMFEFYTWLPEFFPAANIYAQC-DGISPGLFDVLTWLGYNSTMMNPITYP	321					
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
Dd	267	DHKAAITGVGTMGVELICOWPFECVNITYTSYCKTICIGRAFOVLTWLVGSNSAFNPITYS	326					
Qy	322	LEMDFEKALGRPLPCRPCREERQASIASPSLRTSHSGPRRGSLIOO---VLPDLPDPD	377					
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
	:	:::::	:	:	:	:	:	:
Dd	327	IFNFTEFRAEFKRIITKGARANGDP-----TSECGEERSVYVQACRNCSIMECNIISPR	379					







Query Match	22.8%	Score 523.5	DB 5	Length 391
Best Local Similarity	36.3%	Pred No. 1.1e-29		
Matches 125	Conservative 58	Mismatches 126	Indels 33	Gaps 10
QY	8	TANSTPAMGAGPPSADGG-SGVWVAAL----	CVVIALTAANSLLIALICTOPALENTSN	62
DB	17	TANSTEA-SVSGCFAPNPYSAGVQAVLGLITVILITLVIGVAVLVAVTCRKMKMTVTYN	75	

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RESULT      14
098842      PRELIMINARY;      PRT;      445 AA.
ID      098842
AC      098842;
DT      01-FEB-1997 (TREMBLrel. 02, Created)
DT      01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      DOPAMINE D1A2 RECEPTOR,
GN      D1A2.
OS      Anguilla anguilla (European freshwater eel).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC      Anguillidae; Anguilla.
OX      NCBI_TaxID=7936;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97160583; PubMed=9006917;
RA      Cardinaud B., Coudouel S., Vincent J.D., Vernier P.;
RT      "Early emergence of three dopamine D1 receptor subtypes in
RT      vertebrates. Molecular phylogenetic, pharmacological, and functional
RT      criteria defining D1A, D1B, and D1C receptors in European eel Anguilla
RT      anguilla.";
RL      J. Biol. Chem. 272:2778-2787(1997).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL; 062919; AAC60069.1; -.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      InterPro; IPR000209; Peptidase_S8.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHHODPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECP_FL1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECP_FL2; 1.
DR      PROSITE; PS00136; SUBTILASE_ASP_UNKNOWN.1.
KW      G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ      SEQUENCE      445 AA;      49310 MW;      B43ADAB81C1C1439 CRC64;

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	Query Match	22.3%	Score 511.5:	DB 13:	Length 445:
	Best Local Similarity	33.3%	Pred. 8.8e-29:		
	Matches 118:	Conservative 69:	Mismatches 134:	Indels 33:	Gaps 9:
QY	33	LCVVAITAAASLSLIALICTOPALRN-TSNFFVLSTFSDMLGCLVWPPRANLANLYGR	91		
	:   :	:   :	:   :	:   :	:
Dp	28	LSSLIVSTLTGLNTLVCAAVTKFRHLRSKTYNEFVSLAASDILLVALIIVMPKRAVEVAGF	87		
QY	92	WTLARCLCLMTAFDMVCSSATILNCLISLDRIYLILSPRLXYKLRMPLRLALAVLGWM	151		
	:   :	:   :	:   :	:   :	:
Dd	88	WEFG-SFCINIMWAFDMCTASTILNCIIISVDRYMAISSPFERYERKMIPKVAFWVMIVAM	146		
QY	152	SIAAALASFPLILGGHEL-----GARPPVPEQGCLLASLPVVIVASGLTFPLPSG	202		
	: :   :   :   :	: :   :   :   :	:	:	:

Db 147 TSLLSIFIPVQINMHKQTTSEYDHNQSYGDDLLDNCDSLNRTYAISSSLSIFIPVA 206  
QY 203 AICEFTCRILLARKQAVASITTGASQASETLOWPRPREGVESADSRRLATKHSRK 262  
Db 207 IMVTYTRIRIAKQIRRSIALE--RAESAKNRHNSMGNSSSVLESEFSFKSKRETK 264  
QY 263 ALAKTLTGLILGMFTWLPFVAVNYQAVCD-----CISPGLEFDVLTWIGYC 311  
Db 265 VLK---TSLVIMGVFCWMLPFILNCMVPCQAHNGSADPFCVSSSTTFNVFWFGMA 321  
QY 312 NSTMNDIIPLEMRDPRKALGRFLPCPR-CPRERQASLASPSLRTSHSGPRPGI 364  
Db 322 NSSLNPIIY-AFNADPRKAFSILGCHRLCPGNSNAIEIVS----INNNGAPQL 370

QY 336 PCPRCPREQA--SLASP--SL-----RTSHSGPR-----PGLSLQOVLPLP 373  
Db 412 RC-QCRRRRRLWSLRPPLASLDRRRARLRLPQPSHRSPPGSSPHCTPCGGLGR----- 465  
QY 374 LPPDSDSDSAGSG---GSSGLRTLQALL 400  
Db 466 -----HAGDAGFGLOQSKASLRLEWRLL 489

Search completed: March 15, 2002, 14:14:06  
Job time: 211 sec

RESULT 15  
Q9QW71  
ID 09QW71 PRELIMINARY; PRT; 559 AA.  
AC 09QW71;  
RT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ALPHA 1-ADRENERGIC RECEPTOR SUBTYPE ALPHA 1D, ALPHA 1D-AR.  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Rattus;  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92100054; PubMed=1661838;  
RA Perez D.M., Plascik M.T., Graham R.M.;  
RT "Solution-phase library screening for the identification of rare  
RT clones: isolation of an alpha 1D-adrenergic receptor cDNA.";  
RL Mol. Pharmacol. 40:876-883(1991).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 559 AA; 59739 MW; 37CD9BD6D3A47D CRC64;

Query Match 22.2%; Score 509.5; DB 11; Length 559;

Best Local Similarity 33.3%; Pred. No. 1.5e-28;  
Matches 150; Conservative 63; Mismatches 158; Indels 79; Gaps 19;

QY 4 EPGPTA---NSTPAGACPPSPAG-GSGWVAALCVIALTPAANSLLIAL-ICTQPAL 57  
Db 66 EPGMAASGEVNGSAVGLVNSAGVGCVFLAA---FILTRVAGNLLVILSVACNRHL 121  
QY 58 RNTSNEFLVLTSDLMGLVVMPPAMLNALYGRWVLARGLCILMTAFDVMCCASILNL 117  
Db 122 QVTWVFYVNLAVADLLSAAVLPFSATMEVGFNAFGRTFCDVMAAVDVLCTASITSL 181  
QY 118 CLISDRYLLISPLRYKRLMTPLRALALVLGWSLALASFLPLLGGWHELGHARPYP 177  
Db 182 CTISVDRYVGRHSLSKYPALMIERKAAALIALMAVALVSVGP-TLGWKE-----PVP 234  
QY 178 CQ---CRLIASLPVLVAGSLTFPLPSGALCTYCGIILAKRKQAVASLTGMASSQAS 234  
Db 235 PDERFCGITEEYGAIFSSVCSFLPMAYIVMYCRVYVARS---TTRSLERGIKREPQ 291  
QY 235 ETLOV-----PRTPR---PGVESADSRRLATKHSRKAL-----KAKLTGLILGMF 277  
Db 292 KASEVVLRIHCGARTSAKAGYPTQSSKGHFLRSSLSVRLKFSREKKAKTALIVGVF 351  
QY 278 FVTWLPFVAVNYQAVCDISP--GLEFDVLTWIGYCNSTMPNDIIPLEMRDPRKALGRFL 335  
Db 352 VLCWPFEEFVLPFGSIFPQIKPSGVFVFWLGYFNSCVNDLIYPCSSREKRAFLRL 411

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:08:30 ; Search time 14.43 Seconds  
(without alignments)  
686.171 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292

Sequence: 1 MVEPPTANSTPAMGAGPP.....FNIDPAPELRPHPLGIPTN 440

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

212252

Total number of hits satisfying chosen parameters: 212252

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
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5: /cgn2\_6/ptodata/2/1aa/PTOS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	24.3	468	2	US-08-390-000A-7
2	557	24.3	477	1	US-08-087-772A-16
3	554	24.2	405	1	US-08-351-473B-2
4	553.5	24.1	365	2	US-08-467-559B-9
5	552.5	24.1	400	1	US-08-351-473B-5
6	552.5	24.1	400	4	US-08-450-962-4
7	552.5	24.1	400	4	US-08-450-962-6
8	552.5	24.1	446	1	US-07-626-618A-21
9	552.5	24.1	446	1	US-08-333-977-21
10	551.5	24.1	400	1	US-07-916-901-6
11	551.5	24.1	400	1	US-07-783-602C-1
12	551.5	24.1	400	1	US-08-351-473B-4
13	551	24.0	477	1	US-08-444-734A-4
14	547.5	23.9	446	2	US-07-969-267B-4
15	546	23.8	388	1	US-08-087-772A-2
16	538.5	23.5	472	1	US-08-194-338-6
17	533.5	23.3	487	1	US-08-444-734A-2
18	533	23.3	408	1	US-08-351-473B-3
19	531	23.2	402	1	US-08-444-734A-6
20	531	23.2	402	1	US-08-087-772A-15
21	531	23.2	408	4	US-07-916-901-2
22	531	23.2	408	4	US-08-450-962-2
23	531	23.2	408	4	US-08-450-962-5
24	524.5	22.9	446	1	US-07-626-618A-22
25	524.5	22.9	446	1	US-08-333-977-22
26	523	22.8	400	2	US-08-103-170-9
27	515.5	22.5	483	1	US-08-194-338-7

28	508	22.2	559	2	US-08-406-855A-20	Sequence 20, Appl
29	508	22.2	559	3	US-09-206-899-20	Sequence 20, Appl
30	503	21.9	572	1	US-08-334-698-2	Sequence 2, Appl
31	503	21.9	572	1	US-08-228-932-2	Sequence 2, Appl
32	503	21.9	572	1	US-08-468-939-2	Sequence 2, Appl
33	503	21.9	572	1	US-08-722-001-30	Sequence 30, Appl
34	503	21.9	572	2	US-08-406-855A-2	Sequence 2, Appl
35	503	21.9	572	2	US-08-722-190-2	Sequence 2, Appl
36	503	21.9	572	3	US-08-244-354-2	Sequence 2, Appl
37	503	21.9	572	3	US-09-206-899-2	Sequence 2, Appl
38	503	21.9	572	5	PCT-US95-04203-2	Sequence 2, Appl
39	499.5	21.8	501	1	US-08-722-001-14	Sequence 14, Appl
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41	499.5	21.8	501	2	US-09-030-582-9	Sequence 9, Appl
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44	494.5	21.6	478	3	US-09-292-071-33	Sequence 33, Appl
45	494.5	21.6	478	4	US-09-292-069A-33	Sequence 33, Appl

#### ALIGNMENTS

RESULT 1  
US-08-390-000A-7  
; Sequence 7, Application US/08390000A  
; Patent No. 5985583  
; GENERAL INFORMATION:  
; APPLICANT: Seallon, Stuart C.  
; TITLE OF INVENTION: Cloning and Expression of  
; NUMBER OF INVENTIONS: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390,000A  
; FILING DATE: 17-FEB-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 6923-052  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-390-000A-7

Query Match 24.3%; Score 557; DB 2; Length 468;  
Best Local Similarity 33.8%; Pred. No. 96-35;  
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;

QY 1 MVEPPTANSTPAMGAGPPSAPGGSGWVAALCVIALTAANSLLIALICTOPALRMT 60  
DB 24 LVPSPPASTLPPASESPPELSCQWTFAGMLMALIVLLVAGNVIVIAIAKTPRLQTL 83

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OY      61 SNFFVLSFTEDLAWGLVMPAMPALNLYGRWVLARGCLLTMTAFDVMCCSASTLNLCI 120
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
Db      84 TNLFTMSLASADLVWGGLLVFPGATITWVGKHEGSGFCFLMISVDVLCYTASLETLCVI 143
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
OY      121 SLDRYLTLSPLRKKRLMRTPRLALVALYGANSIALASFLPLLGW--HELGHARPPV-- 176
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
Db      144 ALDRLATTSPEFRQSLTRRARAGLVCTVAIAISLVSFLLMHMWRAASDEAKRYND 203
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OY      177 PGOCGLASLPFVVASGLTFEPLGSACIFCYCHILLAAKROAVNAS----LTTGMASQ 232
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
Db      204 PKCDEFVNRAIVAIASSVSSTVFELCMAYVYLNFREDQKVAKKIDSCERRFLGGEPARP 253
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
OY      233 ASET-----LOVPRTPRPVEESADS-----RRLATKHSRKALKAKTLTGIL 273
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
Db      264 PSPSPSPVAPADAPPGPGRPAAAAATAPLANGRAGRKRPSLVALRQKMLK---TLGI 320
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
OY      274 LGMFVTWLFPFVANIQAV-CDICISELPVLTWLGCSNMNPITY---PLFMRFKR 329
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
Db      321 MGVFLLCLPFELLVANVKAFAHRELVPDLRFVFNWLGVAANSAPNPITYCRSP----DFRK 376
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
Db      330 ALGRLLPCRPDPREKQASLASPSLRTSHSGRPGLSLQQVLPULP-PDSPSDSDAASG 388
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
OY      377 AFQGLLCARRAARRRATHDDRRAASGLARFG-----PPSPGASDDDDDDVVGA 429
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|
OY      389 SSGRL 394
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Db      430 TPAPRL 435
        :|::||::|::||::|:|::|||::|::|::|::|::|::|::|::|::|::|::|

RESULT      2
US-08-087-772A-16
; Sequence 16, Application US/0808772A
; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Nahmias, Clara
; APPLICANT: Emoring, Jean L.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
; NUMBER OF INVENTION: Betas-Adrenergic Receptor and Their Applications
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691155th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,772A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Linker, Raymond O.
; REGISTRATION NUMBER: 26,419
; REFERENCE/DOCKET NUMBER: 3339-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-087-772A-16

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Query Match	24.3%	Score 557	DB 1:	Length 477
Best Local Similarity	33.8%	Pred. No. 9.2e35		
Matches 144	Conservative 67	Mismatches 169	Indels 46	Gaps 11

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QY      1 MVEPEPTANSTPAMGAPPPSAPGGSGWVAALCVIALFPAANSLLIALICTOPALRNT 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      33 LVASPPASLILPPASASPEPLSOQWTAGMLMALIVLLIVAGNVLVAIAKTPRIQTL 92
QY      61 SNPEFLSLPESDLMGTVVMPAMUNALYGRVVLARGLCLMTAFDWCSCASILNLCIL 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      93 TNLFLMSLADLVMLVGLVPGATIVYGNREYSGFCELTISVDVLCYASIEETLCVI 152
QY      121 SLDRYLLISPLRYKLDRLMTPRLALALVLGAMSLAALASFLPLLGG--HELGHARPV-- 176
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      153 ALDRYLAITSPEFYQGLLRLRARARGIVCYVAMIALSVSPLPLIMHWMRAFSDEARQYND 212
QY      177 PGGCRLLASLPFLVASGLTFELPSGALCFYTCRLLAARQANOVAS----LTTGASQ 232
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      213 PKCDEFVYTNKAVYIASSVSFYVPLCLIMAFYVLRVREARQKVRKIDSCERRFLGGRP 272
QY      233 ASET-----LQVPTSPRGVESADS-----RLATKRSKALKAKITGL 273
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      273 PPSPPSPVPARAPRPPPPRPAALATAPLANGRACKRRPSRLVALREKALK---TLGII 329
QY      274 LGMFEYTWLPFFVANIYQAV-CDGISPGLEFDVLTWLYGYNSTMDNIY---PLFMRFKR 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      330 MGVEFLCMLPEFLIANVYKAFHRELVDRLFEVFNMLGYANSAFNPIIYCRSP----DFRK 385
QY      330 ALGRFLPCPCREPROASLASPLRSHSGRPRLSLQOVLPLRP-PPDSQSDSADSGG 388
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      386 AFGGLCCARRARRRHHATHGDRPRASGCLARPG-----PPSPGCAASDDDDDYVGA 438
QY      389 SSGRL 394
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      439 TTPARL 444
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      3
US-08-351-473B-2
: Sequence 2, Application US/08351473B
: Patent No. 5656440
: GENERAL INFORMATION:
: APPLICANT: LENZEN, GERLINDA
: APPLICANT: KAPOOR, ARCHANA
: TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
: TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSYADT
: STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/351.473B
: FILING DATE: 21-FEB-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 93 04670
: FILING DATE: 21-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR94/00447
: FILING DATE: 21-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: OBLON, NORMAN F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 6639-001-0X PCT

```

RESULT 4  
US-08-467-559B-9  
Sequence 9, Application US/08467559B  
Patent No. 5928690  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
TITLE OF INVENTION: HUMAN AMINE RECEPTOR  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNER, KESSLER, GOLDSTEIN AND FOX, P.L.L.C  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent-In Dos/Am #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,559B  
FILING DATE: 06-JUN-1995

QY	7	PTANSTPVMGAPSPAPSGSGVAA-----ALCVVIALTPAANSTLIALITCOPALRNTSNF	63
Db	9	PPASLLPPASNSG--SAPLSQQWMTAGMGLVALLVLLVGVGVIVIVAIAKTPRLQTLITNL	66
QY	64	FLVLSFTSDMLVGLVMPMPALNALYGRVLIARGLCLMTAFDVCCSAILNLCLISLD	123
Db	67	FIMSLASADLMGLLVDPGATIVVMGRMEGSEFCELMTISVDLVCTYASIEFTLYIADL	126
QY	124	RYLLLSLRLKLMPTPLRALATLVLGAMSLAAALSFPLLLGW--HELGHARPPV--PCQ	179
Db	127	RYLATISPEFYQSLLTRARALALCTYWAISALVSFLPIIMHMMRAESDEBARCYNDPKC	186
QY	180	CRLASLPEFVIVASGLTFEELPSGAICFTYCHRIILAKROANOVAS-----LTTGMSAQS-	234
Db	187	CDEFTNRRYAIASSVSYFYVLCIMAFYILRVFEADOKYKKIDSCRRFLGGFARPPSP	246
QY	235	ETLOVPRTPRPVESADSR-----RLATKHSKRALAKLTIGILGMEFFVTWLPFEVA	287
Db	247	EPSPSPGPPRPADSLANORSKRRPSRLVALRQGLK---TLGIRMGVFTLCLPFEFLA	303
QY	288	NIYVAQV--CDICISPLLEDVLTWLYGCNSTMNPDIY---PLEMRDFKRLGRLPLCPR---C	340
Db	304	NVYVAFHRLDLPDRLVEFENMLGYANSAFNPDIYCRSP---DFRKAFCORLLCCARRAAC	359
QY	341	PR 342	
Db	360	RR 361	

RESULT 5  
 US-08-351-473B-5  
 : Sequence 5, Application US/08351473B  
 : Patent No. 5656440  
 : GENERAL INFORMATION:  
 : APPLICANT: LENZEN, GERLINDA  
 : APPLICANT: KAPOOR, ARCHANA  
 : TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE  
 : TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS  
 : NUMBER OF SEQUENCES: 9  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: OHLON, SPIYAK, MCLELLAND, MAIER & NEUSTADT  
 : STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
 : CITY: ARLINGTON  
 : STATE: VIRGINIA  
 : COUNTRY: USA  
 : ZIP: 22202  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30

Query Match	24.1%	Score 552.5	DB 1	Length 400
Best Local Similarity	35.1%	Pred. No. 176-34		
-Matches 141, Conservative	60	Mismatches 150	Indels 51	Gaps 15

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Query Match	24.1%	Score 552.5;	DB 4	Length 400;
Best Local Similarity	35.1%	Pred. No. 1.7e-34;		
Matches 141;	Conservative 60;	Mismatches 150;	Indels 51;	Gaps 15;

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OY      5  PGPIANSIPA-WGAGP---PSAPGSGS-----WVAALJCIVIL-?VANAASLIALLCTQ  54
Db      3  PMPHRNSLAMSADAPILDPDPSAANTSGLPGVMAAALAGALLMALATVYGGNLIYIALART  62
OY      55  PALRNTSNFELVSLFTSDLMVGLVMPMPAMINALYGRMVLARGLCLLTWPAFYWCASAST  114
Db      63  PRLOTITWFTVSTLAADIVLIMLMPGATLALTGMHPIGETGCELTMSDVLYCVATSI  122
OY      115  LNLCLISDRLLLSPLRYLRLMTPRLALVLYGAASLAASLFDLLGWHLELGS---  170
Db      123  ETLCALAVDRLATYNTPLRTGTGLTKRRARAAYLVIVISAANSFADJNSOMRWVGADAE  182
OY      171  ---HARPPVQOCRLTASLFEVIVASGLTFEESGAIICEFYCRILLAAKOAQVVASLT  226
Db      183  AQOECHSNRRC---CSFASNMRYALLSSVSRYELPLVLMLEFYARVAVYVARQR- HILARE  238
OY      227  TGMASQASSETLOVPRTRPP-----GVESADR-RLATKHSKAKALITLIGILL  274
Db      239  LGRSPSESPSPSPSPSPSPATGATGPAAPADGPPCGRRPARLLPLREHARL---TGLIIM  295
OY      275  GMFEFTWLPFFVAVNIYQAVC--DCISGLPDEVLTWLTGCTGNSTMPILY---PLFMRFKR  329
Db      296  GIFSLCWLPEFLAVLRLALAGPSLVPSGVFTALMWLTGANSANFNPIYICRSPDFRDAEFR  355
OY      330  AL-----GRFLCPRC---PREQASLASPSLR--TSHSGRP  362
Db      356  LLCSTYGGRPPEEPRAVTFPPASVYAROSPPLNRPDGTGARP  397

```

## RESULT 7

US-08-450-962-6  
: Sequence 6, Application US/08450962  
: Patent No. 6274706  
: GENERAL INFORMATION:  
: APPLICANT: EMORINE, Laurent; MARULLO, Stefano;  
: APPLICANT: STROSBURG, Donny  
: TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND  
: TITLE OF INVENTION: GENES  
: NUMBER OF SEQUENCES: 9  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: KECK, MAHIN & CATE  
: STREET: P.O. BOX 06110  
: CITY: CHICAGO  
: STATE: ILLINOIS  
: COUNTRY: U.S.A.  
: ZIP: 60606-0110  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3-1/2" diskette  
: COMPUTER: IBM compatible  
: OPERATING SYSTEM: MS-DOS  
: SOFTWARE: ASCII  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/450,962  
: FILING DATE:  
: CLASSIFICATION: 530  
: APPLICATION NUMBER: 08/117,829  
: FILING DATE: 08-SEPT-1993  
: APPLICATION NUMBER: 07/721,571  
: FILING DATE: 25-MAY-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: PCT/FR89/00918  
: FILING DATE: 25-JAN-1989  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Fleit, Martin; Gollin, Michael A.  
: REGISTRATION NUMBER: 16,900; 31,957  
: REFERENCE/DOCKET NUMBER: 47078-042  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 789-3400  
: TELEFAX: (202) 789-1158  
: INFORMATION FOR SEQ ID NO: 6:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 400 residues  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: polypeptide  
: DESCRIPTION: polypeptide  
: US-08-450-962-6

Query Match 24.1%; Score 552.5; DB 4; Length 400;  
Best Local Similarity 35.1%; Pred. No. 1.7e-34;  
Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

DB 5 PGPRTNSIPA-WGAGP---PSAPGGSG---WVAALCVVIAL-TAANSLLILICIQ 54  
DB 3 PMPHNGSLALMSDAPRTIDPSAANTSGLPVPMMAALAGALLALATVGGNLLVITAIART 62  
DB 55 PALRNTSNFVLYFTSDLMGLVMPAMLMALYGRVNLARGCLLMTAFDVMCCSASI 114  
DB 63 PRLQITVNFVYSLAAADLVGLVMPGATLALTGHWPLGETGCEIMTVSVLVCVTASI 122  
DB 115 LNLCLISIDRYLLISPLRYKIRMTPLRALALVYLGMSLAALASFLPLLIGHNEG- 170  
DB 123 ETLCLADVRYLAVTNPLRYGTLYTKRRARAVALVLAIVSAVSPAPLMSQWVRGADAE 182  
DB 171 ---HARPVPQCRLLASLPFLVAVSGITFLPSGALCTCYCRILLAAKQAVVASIT 226  
DB 183 AOECHSNPRC---CSFASMPYALLSSVSFLPLLLVLMFLVAVARFYVAKKRR-HLLRE 238  
DB 227 TGMASQASETLVQPTPRP-----GVESADR--RLATKSKRAKAKKLLGLL 274  
DB 239 LGRFSPESPSPSPSPSPATGTPAARDGVPCCGRPARLLRLREHRLR---TLGLIM 295

DB 275 GMFVYTWLPFVANTVOAVC--DCISPLGFDVLTWLGCONSMPLIY---PLFMRDKR 329  
DB 296 GIFSLCMLPFLFANVLRALAGPSLVSGVFLANLWGTANSFNFVITVCRSPDFDARR 355  
DB 330 AL---GRFLPCPRC---PREROASLASPSLR--TSHSGPRP 362  
DB 356 LLCYSGRGPRPEPRAVTFPASPVEARQSPPLNRFQYEGARP 357

RESULT 8  
US-07-626-618A-21  
: Sequence 21, Application US/07626618A  
: Patent No. 5422265  
: GENERAL INFORMATION:  
: APPLICANT: Van Tol, Hubert H.M.  
: APPLICANT: Civelli, Olivier  
: TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses  
: NUMBER OF SEQUENCES: 22  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Allegretti & Witcoff, Ltd.  
: STREET: 10 South Wacker Drive, Suite 3000  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: USA  
: ZIP: 60606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/626,618A  
: FILING DATE: 7 DEC 1990  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: No. 5422265nan, Kevin E  
: REGISTRATION NUMBER: 35,303  
: REFERENCE/DOCKET NUMBER: 90,1092  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 312-715-1000  
: TELEFAX: 312-715-1234  
: TELEX: 810-221-8317  
: INFORMATION FOR SEQ ID NO: 21:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 446 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: HYPOTHEICAL: NO  
: US-07-626-618A-21

Query Match 24.1%; Score 552.5; DB 1; Length 446;  
Best Local Similarity 31.2%; Pred. No. 1.9e-34;  
Matches 143; Conservative 79; Mismatches 172; Indels 65; Gaps 13;

DB 21 SAPGSGWV-----AAALCVIALTAANSLLIALICTPALRN-TSNFFVSL 68  
DB 7 SAMDGTGLVERDFESVRIITACFLSLIILITLIGMTLVCAAVIRRIILRSKVTNFFVSL 66  
DB 69 FTSDLVGLVMPAMLMALYGRVNLARGCLLMTAFDVMCCSASINCLISDRYLI 128  
DB 67 AVSDLLVAVLMPKAVAEIACFPFG--SFCNIMVAFDICTASTILNLCVLSVDRIAT 125  
DB 129 LSPRLRYKIRMTPLRALALVYLGMSLAALASFLPLLIGHNEGHLHARPVPG----- 178  
DB 126 SSPFYERKMTKAPFILLISVAMTISVLSIFPVQLSMHK---AKPTSPSDGNATSLAET 182  
DB 179 ---QCRLASLPFLVAVSGITFLPSGALCTCYCRILLAAKQAVVASL-TTGMASQASE 235  
DB 183 IDNCDSLSRTYAISSVSIFYIPVAIMVTVTRYRIAOKIRRIALERAHAHAKNQ 242





Matches	144;	Conservative	61;	Mismatches	146;	Indels	51;	Gaps	15;
QY	5	PGPIAINTSIPA-WGAGE---	PSAPGSGG----	WVAALCIVTAL--TAAANSLLIALICTQ	54				
Dd	3	PWPHKNGSLAEWSDAPITDPSAANTSGLPGVFWAAALAGALLATLVGCGNLLITAIART			62				
QY	55	PALRNTSNFVLVSFTSDLMWGLVYMPRAMLNATLGRVNLACGLCLLTWTAIPFYMCSSASI			114				
Dd	63	PRLOITIVFVTSIATADLVGGLVMPWGATLALGHPMLGATGCELMWTSYVULCVTSASI			122				
QY	115	LNLCLISIDRLLLISPLRYKRMTRRLALALVGLAMSLAALASFLPLLLIGMHEG----			170				
Dd	123	ETLLCALADRYLAVINPLRYGTLYVKKRRARAIVLVWIVTASVVSAPINSMQWRVGADAE			182				
QY	171	----HARPPVGQGRLLASLPFLVLAAGTFLPLPSGALCFCTYCRILLAAKROAVOV----			222				
Dd	183	AOECHSNRC---CSFASNMPPALSSSVSYFLPLVLMLETVARFVAAKRRPRRYRRL			239				
QY	223	-----ASLTIGMASQASETLOVPRTPPRGVESADSR--RLATKHSRKALAKLTGLIL			274				
Dd	240	GRFPPEESPRSRSPSPATVGTPTADGDVSCGRRRARLLRPLGEHRALR---TLGLIM			295				
QY	275	GMFEVTLWLPFVAVANTQAVC--DCISPGLEFVLTWLYGYCNSTMNPILY--PI			329				
Dd	296	GIFSLCWLPEFLANLVRALVGPISLVPSGVALILNMLGYANSAFNPLIYCRSPDFRDAFR			355				
QY	330	AL-----GRFLFCPRC---PREQASLASPSLR--TSHSFRP			362				

RESULT 12  
US-08-351-473B-4  
: Sequence 4, Application US/08351473B  
: Patent No. 5656440  
: GENERAL INFORMATION:  
: APPLICANT: LENZEN, GERLINDA  
: APPLICANT: KAPOOR, ARCHANA  
: TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE  
: TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS  
: NUMBER OF SEQUENCES: 9  
: CORRESPONDENCE ADDRESS:  
: ADDRESS: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT  
: STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
: CITY: ARLINGTON  
: STATE: VIRGINIA  
: COUNTRY: USA  
: ZIP: 22202  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/351,473B  
: FILING DATE: 21-FEB-1995  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 93 04670  
: FILING DATE: 21-APR-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: PCT/FR94/00447  
: FILING DATE: 21-APR-1994  
: ATTORNEY/AGENT INFORMATION:  
: NAME: OBLON, NORMAN F.  
: REGISTRATION NUMBER: 24,618  
: REFERENCE/DOCKET NUMBER: 6639-001-0X PCT  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (703) 413-3000  
: TELEFAX: (703) 413-2220  
: TELEX: 248855 OPAT UR  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:

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; LENGTH: 400 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-351-473B-4

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Query Match	24.1%	Score 551.5	DB 1	Length 400
Best Local Similarity	35.1%	Pred. No. 2e-34		
Matches 141, Conservative	62	Mismatches 148	Indels 51	Gaps 15

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0Y 5 PGPANSPPA-WGAGP---PAPGSG-----WVAALCVIAL-TPAANSLIALICQ 54
Db 3 PMPHKNGLAWSDAPPLIDPSAANTSGLPVPMAAALAGALLALATYAGMLVITTAIRT 62
0Y 55 PALRNTSNFLLVSETSDUMVGLVYMPMAMINALYGRWVLARGICLLMTAFDYWCSCASI 114
Db 63 PRLQITVFWFVTSLATADLVGLLWMPGATLITGHMPLGATCELMTSVDVLCVYASI 1222
0Y 115 LNLCLISIDRLLLLLSPTRYLKRTPPLRALALVIGANSALALASFELLLGWHELG---- 170
Db 123 ETLCALAVDRILATVNPRLRGVLTLYKRRARAAYLVIVASATVSFAFIMSQMRVGDADAE 1820
0Y 171 ----HARPPVPGOGRLLASLPFVYASGLFPELPSGAICTFYCHLLAKOAVNASLT 226
Db 183 AOECHSNRC--CSFASNMPLYALLSSVSSTYELPLVYLAVYAVFVAVARQR-RLRRE 238
0Y 227 TGMASOASETLQVPRTPP-----GESADSR-RLATKHSRKALKAKLTIGLIL 274
Db 239 LGRPPEESPRSPSPSPATVYGTPTASDGVPSGCRPRALLPLGEHRALR---TTLGIM 295
0Y 275 GMFEVYTWLPFFVANIIVQAVC--DCISPLEDVLTWLGYCNSTNMPITY---PLEMRDKR 329
Db 296 GIFSCWLPFFELAVIRALVSPSLVPSGVTALMLWLGIVANSANFPLIYCRSPDFDAEFR 355
0Y 330 AL----GRFLCPRC---PRRROASLASPSLUR--TSHSGPRP 362
Db 336 LLCSTGGGPEEPKRVYTFPASVPAVSROKSPLNMRFDGVEGEP 397

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RESULT 13  
 US-08-444-734A-4  
 : Sequence 4, Application US/08444734A  
 : Patent No. 5610282  
 : GENERAL INFORMATION:  
 : APPLICANT: Sibley, David R.  
 : APPLICANT: Monsma, Frederick J.  
 : APPLICANT: Mahan, Lawrence C.  
 : APPLICANT: McVittie, Loris D.  
 : TITLE OF INVENTION: cdna encoding the rat D1 dopamine  
 : TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and  
 : TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected  
 : TITLE OF INVENTION: cell lines  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Knobbe, Martens, Olson and Bear  
 : STREET: 620 Newport Center Drive, Sixteenth Floor  
 : CITY: Newport Beach  
 : STATE: CA  
 : COUNTRY: USA  
 : ZIP: 92660  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/444,734A  
 : FILING DATE:  
 : CLASSIFICATION: 530  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/029,917

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1      BILLING DATE: 03-MAR-1993
2
3      PRIOR APPLICATION DATA:
4
5      APPLICATION NUMBER: US 07/548,714
6
7      FILING DATE: 06-JUL-1990
8
9      ATTORNEY/AGENT INFORMATION:
10
11      NAME: Altman, Daniel E.
12
13      REGISTRATION NUMBER: 34,115
14
15      REFERENCE/DOCKET NUMBER: NIH065.001FW
16
17      TELECOMMUNICATION INFORMATION:
18
19      TELEPHONE: (714) 760-0404
20
21      TELEFAX: (714) 760-9502
22
23      INFORMATION FOR SEQ ID NO: 4:
24
25      SEQUENCE CHARACTERISTICS:
26
27      LENGTH: 477 amino acids
28
29      TYPE: amino acid
30
31      STRANDEDNESS: single
32
33      TOPOLOGY: linear
34
35      MOLECULE TYPE: protein
36
37      HYPOTHETICAL: NO
38
39      ANTI-SENSE: NO
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41      FRAGMENT TYPE: internal
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Query Match	24.0%	Score 551	DB 1	Length 477
Best Local Similarity	33.8%	Pred. No. 2.6e-34		
Matches 144; Conservative	66;	Mismatches 170;	Indels 46;	Gaps 11

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0Y      1 MVEPEGFPA NSTPAMGAGPPSPAGSGGVAALCCVIALTRPAAASLLIILICHOPLARNT 60
Db      33 LVPPASPPASLLPPASSESEPEPLISQOWTGKMLMALIELLIYAGVNLIVAI AKTPRIQTL 92
0Y      61 SNFFLVSLFTSDLMVGLVMPDAMLNALYGRWVLARGCLIMTA FVDMCCSATLNLCT 120
Db      93 TNEIEMSLASLDLWGLLVGFATIVWGGEWSEFCELMISVDVLCTIASIETLCVI 152
0Y      121 SLDERVLLSLRKTIRMTPLRALATLVGMSLAAALSFLPILIGW--HELGHARPPV-- 176
Db      153 ALDRLLATTSPEFRQSLITTRARAGLCYTAISALVSFLPIIMHWRAESDEARCYND 212
0Y      177 PGQGRLLASLPFVLVASGLFFELPSGAICTEYCRILLARQAVQVS---LTTGMSAQ 232
Db      213 PKCDEVTNRAVYLAIVASSVSYFVLCIMAFYLVREPDAGQYVKINDSCERRFLGPARP 272
0Y      223 ASET-----LQYPRTPRCVEGADS-----RLATKSHSKALKAKLTIGIL 273
Db      273 PSPSPVPAPADAPPGPGRPAAATAATAPLANGRAGKRRSPSLVARBOKAL--TLGII 329
0Y      274 LGMEFVTVLPPEFVANIYQAV--CDCISGCLFVNLVWLGKNSNTMPRIY---PLEMPDRFKR 329
Db      330 MGVETTLCLHLPFLANVYKAFIRELVPDRLEVPFFNMWLGYSANAFNPITYCSP----DFRK 365
0Y      330 ALGRFLPCPCPRERQASLASPSLRTSHSGRPGLSLQOVLPLPLP--PDSDSODSDAGSGG 388
Db      386 AFQGLLCCARRAARRRHATHGDPRRAGSLARP-----PPSPCAASDODDDDDVVGA 438
0Y      389 SSGURL 394
Db      439 TTPARL 444

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RESULT 14  
US-07-969-267B-4  
Sequence 4, Application US/07969267B  
Patent No. 5862835  
GENERAL INFORMATION:  
APPLICANT: Weinstein, Richard L.  
APPLICANT: Hartig, Paul R.  
TITLE OF INVENTION: DNA Encoding A Human Dopamine D1  
RECEPTOR  
TITLE OF INVENTION: Receptor And Uses Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/969,267B  
FILING DATE: 05-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/551,448  
FILING DATE: 10-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37526-A-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: D1  
US-07-969-267B-4

Query Match 23.9%; Score 547.5; DB 2; Length 446;  
Best Local Similarity 30.9%; Pred. No. 4,4e-34;  
Matches 142; Conservative 80; Mismatches 172; Indels 65; Gaps 13;

21 SAPGSGWV-----AAALCVIALTAANSLIALICTOPALRN-TSNEFLVSL 68  
7 SAMDTGLVERDFSVRLITACFLSLILLTLLGNTLVCAAVIRFRLRSKYTNFVLSL 66  
69 FTSIDLAVGIVPMPMLNLYGRWYLARGLCLMTAFDVMCCSASLNLCLISDRYLLI 128  
67 AVSDLLVALVLPWKRAVEIAGFWPG-SFCNIMWAFDLMCTASTILDLCVIVDRYMAI 125  
129 ISPLRYKLMPTLRALAVLIGAMSLAALASFLPLLGWHELGHARPPVG----- 178  
126 SSPEYERKMTKAFILISVAMTSLVLSIFIPVQLSMHK---AKPTSSDGNATSLAET 182  
179 --QCRLASLPFVLVAGITFFLPAGAICTFYCRILLAAKQAVOYASL--TTGMAQASE 235  
183 IDNCSSSLSRFYAISSVISFYIPVAIMIVTYTRYIRIAOKOIRRIALALERAHVAKNQ 242  
236 TLQVTRTPGVESADSRSLATKHSRKALKAKLTGLIGMFVWLPFEVANIYQAVSD 295  
243 TTGNGKPEGSCOPSSSEKMSFKRETLYLK---TLVLMGVVCCMLPFLINCLIPFG 299  
236 -----CISPLGLFVLITWLGYNSTMPNIIPLFMRDGRALGRFLPCPR-CPERQA- 346  
300 SGEOTPCIDSTFPFVFWGANSINPIIY-AFNADRKAFSTLLGCRYLCPATNNMI 358  
347 -----SLASPSLRTSHSGRPLSLQOVLPLPPDSODSDAGSGGSGGLRLTAQLLLP 401  
359 ETVSINNGAAMFSSHHEKRGISKECNLYLIPHAVGSSSEDLKKEAGIARPLEKISP 418  
402 GEATQDPLPTRAAAVNFENIDPAEPLRP-----HP 434  
419 -----ALSVILDYDTVDSELEKIQPTONGQHP 445

RESULT 15  
US-08-087-772A-2  
Sequence 2, Application US/08087772A  
Patent No. 5691155  
GENERAL INFORMATION:  
APPLICANT: Nahmias, Clara  
APPLICANT: Emorine, Jean L.  
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine  
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5691155th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,772A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Linker, Raymond O.  
REGISTRATION NUMBER: 26,419  
REFERENCE/DOCKET NUMBER: 3339-195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-087-772A-2

Query Match 23.8%; Score 546; DB 1; Length 388;  
Best Local Similarity 35.9%; Pred. No. 5e-34;  
Matches 139; Conservative 59; Mismatches 137; Indels 52; Gaps 16;

5 PGPTANSTPA-MGAGP---PSAPGSGG-----WAAALCVIAL--TAANSLIALICTQ 54  
3 PMPHRGSLALNSDAPTLPSSAANTSGLPVPMALAGALLALAVGNNLLVLIART 62  
55 PALRNTSNFLVSLFTSDMLVGVMPMLNLYGRWYLARGLCLMTAFDVMCCSASI 114  
63 PRIQTTNVEFVSLAADAIVGVLPMPGATLALTGHPGLGETGCEIANTSVDLCTASI 122  
115 LNLCLISDRYLLISPLRYKLMPTLRALAVLIGAMSLAALASFLPLLGWHELG----- 170  
123 ETLCALAVRYLAVTNPLRYKLTGTLVTKRRRAAVLVMIYSAVSPFPHISQNRVADA 182  
171 ----HARPPVQOCRLASLPFVLVAGITFFLPAGAICTFYCRILLAAKQAVOYASLT 226  
183 AQECHSNPRC---CSFASNMYPALLSSVSFYLPFLVLMFVYARVAVAKRQ-HLRRE 238  
227 TGMASQASTETQVPTPRP-----GVESADR--RLATKHSRKALKAKLTIGILL 274  
239 LGRFSPESPPSPSRSPATGTPAAPDGVPPCGRRPARLLPLREHRLR---TLGLIM 295  
275 GMEFVTLPEFVAVNTVOAC--DCISPLGLFVLITWLGYNSTMPNIIY---PLFMDFKR 329  
296 GLFSLCMLPEFLANVRLALAGPSLVPSGVFIALNWLGTANSAPNVIYCRSP---DFRD 351  
330 ALGRFLPCP---RCPRERQASL--ASP 351

Db 352 AFRLL-CSYGGGPEPPRAVTFPASP 377

Search completed: March 15, 2002, 14:10:25  
Job time: 115 sec